

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 13, 2006, 13:40:22 ; Search time 194 Seconds
(without alignments)
723.533 Million cell updates/sec

Title: US-10-510-941-2
Perfect score: 1542
Sequence: 1 LETLLEKNVSKTIRGKKII.....KSLDRFLEITADKERAQHV 307

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_8:*

- 1: Geneseq1980s:*
- 2: Geneseq1950s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*
- 9: Geneseq2005s:*
- 10: Geneseq2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1542	100.0	307	7	ADN97355 B. lichen
2	738.5	47.9	310	8	ADS27585 Bacterial
3	734	47.6	301	5	ABBA74777 Listeria
4	734	47.6	301	6	ABU32480 Protein e
5	639	41.4	306	5	ABBA48180 Listeria
6	638	41.4	309	8	ADG32114 Mutant B
7	536	34.8	302	6	ABU44428 Protein e
8	535.5	34.7	306	8	ADS28089 Bacterial
9	516	33.5	299	8	ADN27185 Bacterial
10	501	32.5	311	8	ADNA48041 Thermococ
11	493	32.0	306	8	ADS41933 Bacterial
12	493	32.0	308	8	ADN18644 Bacterial
13	491.5	31.9	308	8	ADN18683 Bacterial
14	490	31.8	309	8	ADNA46530 Thermococ
15	485	31.5	221	8	ADS27537 Bacterial
16	484.5	31.4	308	10	AEBS95518 E. faecal
17	474.5	30.8	322	8	ADNA46418 Thermococ
18	473	30.7	305	4	ABBS6628 Putative
19	473	30.7	305	8	ADS43172 Bacterial
20	455.5	29.5	306	6	ABU25506 Protein e
21	455.5	29.5	310	7	ADCS97283 E. faeciu
22	451.5	29.3	325	4	ABBS6710 Putative
23	451	29.2	300	5	ABP26280 Streptoco

24	447.5	29.0	285	6	ABU26098 Protein e
25	447.5	29.0	377	6	ADN11670 Alloiooc
26	444	28.8	328	8	ADN46668 Thermococ
27	442	28.7	300	5	ABP26335 Streptoco
28	442	28.7	300	8	ADV88530 Streptoco
29	442	28.7	300	8	ADV81939 Streptoco
30	442	28.7	300	8	ADV79783 Streptoco
31	438	28.4	311	8	ADS22213 Bacterial
32	436	28.3	233	5	ABBS9645 Amino aci
33	436	28.3	233	6	ADG72543 Streptoco
34	436	28.3	233	8	ADU80820 MutF, SEQ
35	435.5	28.2	297	8	ADS29173 Bacterial
36	434.5	28.2	305	8	ADN47270 Thermococ
37	432.5	28.0	310	6	ABU24420 Protein e
38	431.5	28.0	305	8	ADS29082 Bacterial
39	431.5	28.0	316	8	ADS29721 Bacterial
40	430.5	27.9	233	8	ADS22132 Bacterial
41	430.5	27.9	332	7	ADCS94125 E. faeciu
42	429	27.8	312	4	AAG92767 C glutami
43	428.5	27.8	306	8	ADN46278 Thermococ
44	425	27.6	308	8	ADS27622 Bacterial
45	424.5	27.5	312	8	ADN18549 Bacterial

ALIGNMENTS

RESULT 1
ADN97355
ID ADN97355 standard; protein; 307 AA.
AC ADN97355;
XX
XX
DT 01-JUL-2004 (first entry)
XX
DE B. licheniformis antibiotic synthesis related protein SEQ ID NO:2.
XX
KW antibiotic synthesis; proteolytic; protease.
XX
OS Bacillus licheniformis.
XX
PN WO2003087142-A2.
XX
PD 23-OCT-2003.
XX
PP 25-MAR-2003; 2003WO-DK000199.
XX
PR 10-APR-2002; 2002DK-00000532.
XX
PA (NOVO) NOVOZYMES AS.
XX
PI Andersen JT, Jorgensen ST, Raemussen MD, Olsen PB, Clausen IG;
DR WPI; 2003-833704/77.
DR N-PSDB; ADN97354.
PT New Bacillus licheniformis mutant host cell that is mutated in one or
PT more gene(s) encoding one or more polypeptide(s) having proteolytic
PT activity, useful for producing, isolating and/or purifying at least one
PT product of interest.
PS Disclosure; SEQ ID NO 2; 100pp; English.
CC The invention relates to a novel Bacillus licheniformis mutant host cell
CC derived from a parent B. licheniformis host cell, where the mutant host
CC cell is mutated in one or more gene(s) encoding one or more
CC polypeptide(s) having proteolytic activity that is at least 80% identical
CC to any of the 22 amino acid sequences fully defined in the specification,
CC where the mutant host cell expresses at least 5% less of one or more
CC polypeptide(s) having a proteolytic activity than the parent host cell,
CC when they are cultivated under comparable conditions. The host cell is
CC useful for producing at least one product of interest, and for isolating
CC or purifying the product of interest. The present sequence represents an

Handwritten signature

CC antibiotic synthesis related polypeptide of the invention.

XX
SQ Sequence 307 AA;

Query Match 100.0%; Score 1542; DB 7; Length 307;
Best Local Similarity 100.0%; Pred. No. 3e-130;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LETLLEKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGAGTITIRIMVGHMSITAGE 60
DB |||||
QY 1 LETLLEKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGAGTITIRIMVGHMSITAGE 60
DB |||||
QY 61 IAVCGSVKENFEKAAHIGAIIVENPELYKFLTGYNLQOYARMTKGVTKKIDIEIVELV 120
DB |||||
QY 61 IAVCGSVKENFEKAAHIGAIIVENPELYKFLTGYNLQOYARMTKGVTKKIDIEIVELV 120
DB |||||
QY 121 GLKNRINDKVYSLGMRORGLAQSLHDPKLLIIDEPTNGLDPAGIREIRDYLRKLT 180
DB |||||
QY 121 GLKNRINDKVYSLGMRORGLAQSLHDPKLLIIDEPTNGLDPAGIREIRDYLRKLT 180
DB |||||
QY 181 EKGMAVIVSHLLSEMELMCDRTAIIQNGKLRDIQHVHGPARDKKRYIIQADDTQALTR 240
DB |||||
QY 181 EKGMAVIVSHLLSEMELMCDRTAIIQNGKLRDIQHVHGPARDKKRYIIQADDTQALTR 240
DB |||||
QY 241 EAAAFKRVKVDKAEAGGIELSIQKDEVPDLIKHLTDSGVRLYEYKAVNKSLEDRFLITAD 300
DB |||||
QY 241 EAAAFKRVKVDKAEAGGIELSIQKDEVPDLIKHLTDSGVRLYEYKAVNKSLEDRFLITAD 300
DB |||||
QY 301 KEEAQHV 307
DB |||||
QY 301 KEEAQHV 307
DB |||||

RESULT 2
ADS27585 standard; protein; 310 AA.

XX AC ADS27585;
XX DT 02-DEC-2004 (first entry)
XX DE Bacterial polypeptide #16618.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX Bacteria.
XX OS
XX US2003233675-A1.
XX PN
XX 18-DEC-2003.
XX PD
XX 20-FEB-2003; 2003US-00369493.
XX PF
XX 21-FEB-2002; 2002US-0360039P.
XX PR
XX (CAOV//) CAO Y.
XX PA (HINK//) HINKLE G J.
XX PA (SLAT//) SLATER S C.
XX PA (CHEN//) CHEN X.
XX PA (GOLD//) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 16618; 122pp; English.

XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 310 AA;

Query Match 47.9%; Score 738.5; DB 8; Length 310;
Best Local Similarity 48.5%; Pred. No. 7.8e-58;
Matches 147; Conservative 66; Mismatches 81; Indels 9; Gaps 3;

QY 1 LETLLEKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGAGTITIRIMVGHMSITAGE 60
DB |||||
QY 10 MTTILSVRLDKKIVIGKKTIVENISFDVKGQEVFGFLGPNAGAGTITIRMLVGLIKATEGT 69
DB |||||
QY 61 IAVCGSVKENFEKAAHIGAIIVENPELYKFLTGYNLQOYARMTKGVTKKIDIEIVELV 120
DB |||||
QY 70 ISIGYSIKENFREAMRQIGSIVENPELYTILTGWENLAKQFARMGLGDISERIEIAEMV 129
DB |||||
QY 121 GLKNRINDKVYSLGMRORGLAQSLHDPKLLIIDEPTNGLDPAGIREIRDYLRKLT 180
DB |||||
QY 130 HLDERIHDKVKTYSYLGMRORGLAQSLHDPKLLIIDEPTNGLDPAGIREIRDYLRKLT 189
DB |||||
QY 181 EKGMAVIVSHLLSEMELMCDRTAIIQNGKLRDIQHVHGPARDKKRYIIQADDTQOA 237
DB |||||
QY 190 EENMSVFISSHLLSEVQMICDRVAIIHKGMITVAKVEELIKTASDRVEWIVTPISKAKD 249
DB |||||
QY 238 LTREAAAFKRVKVDKAEAGGIELSIQKDEVPDLIKHLTDSGVRLYEYKAVNKSLEDRFL 295
DB |||||
QY 250 MLEAAKEVREVSVE----GDRLLCRMDIASISSWKNKHFEVNEIDVHVKELVFTLEDLFI 305
DB |||||
QY 296 EIT 298
DB |||||
QY 306 ELT 308
DB |||||

RESULT 3
ABB47477
ID ABB47477 standard; protein; 301 AA.

XX
AC ABB47477;
XX
DT 05-FEB-2002 (first entry)
XX
XX Listeria monocytogenes protein #181.
XX
XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
XX vitamin B12; bacterial infection; disease.
XX

OS Listeria monocytogenes.

XX PN WO200177335-A2.
XX PD 18-OCT-2001.
XX PF 11-APR-2001; 2001WO-FR001118.
XX PR 11-APR-2000; 2000FR-00004629.
XX PA (INSP) INST PASTEUR.
XX PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Feihl H, Dehoux P;
PI Dussurget O, Chetoui F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kref J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX DR WPI; 2002-010914/01.
XX PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
XX PD and prevention of Listeria and related bacterial infections, and related
XX PT polypeptides.
XX PS Claim 6; SEQ ID NO 182; 192pp; French.
XX CC The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccine compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 301 AA;
Query Match 47.6%; Score 734; DB 5; Length 301;
Best Local Similarity 49.8%; Pred. No. 1.9e-57;
Matches 149; Conservative 61; Mismatches 81; Indels 8; Gaps 3;
QY 2 ETTLELNKWSKTIRKKGITGLSFDVRAGIFGLGPNAGKTTTIRMIVGHMSITAGEI 61
DB 3 ERALQTNLHKTKREILNGISFVWMPGEVDFGLGPNAGKTTTIRMIVGLIKPSGTI 62
QY 62 AVCVSVKNEFKAARHGAIVENPELYKFLTCYQNLQOYARMKGVTKKKIDEIVELVG 121
DB 63 LIGGKDIRKNFTAMRGLGSIVENPEFTLTQENLAVFARMDSIKKERIQEVTELVG 122
QY 122 LKRRINDKVTYSLGNRORLGAOSLLHDPKLLILDEPTNGLDPAGIREIRDLVKLTRE 181
DB 123 LKRRINDRSTVSLGNRORLGAOSLLHDPKLLILDEPTNGLDPAGIREIRDLVKLTRE 182
QY 182 KGMNVSVSHLLSEMELMCDRIAIIONGK-LRDIQHVHGPARCKRYITQADDTQALTR 240
DB 183 EGISVLVSHLLSEIELLDCRVAIMTDGTTIKTDQVAHLLSSRAQLRWVTP-----TE 236
QY 241 EAAAF-RKKVDBAEGGIELSIQKQVPLIKHLTDSGVRLVYEVKAVNKSLDRPLEIT 298
DB 237 QAKAFLESVTEVDEYLVLTAMNEESAENQELVAKGIKVHEIDKRPKSLDFLELT 295

RESULT 4

ABU32480
ID ABU32480 standard; protein; 301 AA.
XX AC ABU32480;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #18007.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Listeria monocytogenes.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362899P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX DR WPI; 2003-029926/02.
XX DR N-PSDB; ACA36350.
XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX PD for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX PS Claim 25; SEQ ID NO 60404; 1766pp; English.
XX CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC on a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

```

XX Sequence 301 AA;
SQ
Query Match 47.6%; Score 734; DB 6; Length 301;
Best Local Similarity 49.8%; Pred. No. 1.9e-57;
Matches 149; Conservative 61; Mismatches 81; Indels 8; Gaps 3;

QY 2 ETLLEKNVSKTIRGKIIEGLSFDVRAGEIFGLPGNGAGKTTTIRMIVGHMSITAGEI 61
DB 3 ERALQVNLHKKIRKEIKIGISFEVWPGEVFGFLPGNGAGKTTTIRMIVGLIKPISGTI 62

QY 62 AVCGSVSKENFEKAARHIGAIIVENPELYKFLTYQNLQOQYARMTKGVTKKKIDEIVELV 121
DB 63 LIGGKDIRKNTFTEAMRGLSGIVENPEFYTLTGOENLAVFARMDSIIKKERIQEIVELV 122

QY 122 LKNRINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAQIREIRDYLRKLTRE 181
DB 123 LKXLRINDRVSTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPSGIGHENRDFIRALRN 182

QY 182 KGMVIVSSHLLSEMELMCDRIATIQNGK-LRDIQHVHGPARDKKRYIQADDTQALTR 240
DB 183 EGISVLVSSHLLSEIELLDCDRAIMTDGTIIKTDOVAHLLSSRAQLRWVTP-----IE 236

QY 241 EAAAF-RKKVDBAEGGIELSIQKDEVPDLIKHLTDSGVRLYEYKAVNKSLEDRFLEIT 298
DB 237 QAKAFLESVTEVEVDGELYVTANNEESAENWQNLVAKGIKVHIDKRPKSLEDFLEIT 295

RESULT 5
ABB48180
ID ABB48180 standard; protein; 306 AA.
XX
AC ABB48180;
XX
DT 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes protein #884.
XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.
XX
OS Listeria monocytogenes.
XX
WO200177335-A2.
XX
18-OCT-2001.
XX
11-APR-2001; 2001WO-FR001118.
XX
11-APR-2000; 2000FR-00004629.
XX
(INSP ) INST PASTEUR.
XX
XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Faihi H, Dehoux P;
PI Dusauret O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Donnann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Fortillo F, Gomez-Lopez N;
PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX
XX WPI; 2002-010914/01.
XX
XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and related
PT polypeptides.
XX
XX Claim 6; SEQ ID NO 885; 192pp; French.
XX
XX The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.

```

```

CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 306 AA;
Query Match 41.4%; Score 639; DB 5; Length 306;
Best Local Similarity 45.3%; Pred. No. 7.1e-49;
Matches 135; Conservative 57; Mismatches 104; Indels 2; Gaps 2;

QY 2 ETLLEKNVSKTIRGKIIEGLSFDVRAGEIFGLPGNGAGKTTTIRMIVGHMSITAGEI 61
DB 3 ETVLLEHVTKIKIGKNIVHDSFIDHKGEVFGFLPGNGAGKTTTIRSIIVGLIRREGTV 62

QY 62 AVCGSVSKENFEKAARHIGAIIVENPELYKFLTYQNLQOQYARMTKGVTKKKIDEIVELV 120
DB 63 FINGKNVDTEYKAAISEVCAIIEPEFYMYMSWANLQFARMSQKNITDEHIREIVELV 122

QY 121 GLKNRINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAQIREIRDYLRKLT 180
DB 123 KLTGAINQKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAQIREIRDYLRKLT 181

QY 181 EKGMAVIVSSHLLSEMELMCDRIATIQNGKLRDIQHVHGPARDKKRYIQADDTQALTR 240
DB 182 TNGTSVLISLSSHLLSEIQITDRPAIINKGVLTTHIEKMSDLIENHVAAYKLVSDPVATTT 241

QY 241 EAAAF-RKKVDBAEGGIELSIQKDEVPDLIKHLTDSGVRLYEYKAVNKSLEDRFLEIT 298
DB 242 VLATLPVKLVQNEIDLKIEVAHEDVHLIARALIQANIDLELVPLQASLEERFLEIT 299

RESULT 6
ADG32114
ID ADG32114 standard; protein; 309 AA.
XX
AC ADG32114;
XX
DT 26-FEB-2004 (first entry)
XX
DE Mutant B_licheniformis secreted polypeptide Seqid 84.
XX
KW mutant; host cell; production yield; shelf life; product stability;
KW purity; secreted; mutein.
XX
OS Synthetic.
XX Bacillus licheniformis.
XX
WO2003093453-A2.
XX
13-NOV-2003.
XX
25-MAR-2003; 2003WO-DK000198.
XX
10-APR-2002; 2002DK-00000534.
XX
(NOVO ) NOVOZYMES AS.
XX
Andersen JT, Jorgensen ST, Rasmussen MD, Olsen PB, Clausen IG;
XX WPI; 2004-053045/05.
XX N-PSDB; ADG32113.

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Db 241 MRKGFEEBNSQIVLKDYNKNTIAAAVKVLVANDIIDYQVRMVRKSLEBVFDMT 295

RESULT 8

ADS28089

ID ADS28089 standard; protein; 306 AA.

XX ADS28089;

XX

XX

XX 02-DEC-2004 (first entry)

XX Bacterial polypeptide #17122.

XX

XX Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

KW pathogen tolerance; pest tolerance; plant disease resistance;

KW cell cycle pathway modification; plant growth regulator;

KW homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

KW bacterial polypeptide.

XX Bacteria.

OS US2003233675-A1.

PN 18-DEC-2003.

PD

XX 20-FEB-2003; 2003US-00369493.

PF

XX 21-FEB-2002; 2002US-0360039P.

PR

XX (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

PI WPI; 2004-061375/06.

XX

XX New recombinant DNA construct comprising a promoter positioned to provide

PT for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.

XX

XX Claim 1; SEQ ID NO 17122; 122pp; English.

PS

XX The invention relates to a recombinant DNA construct comprising a

CC promoter functional in a plant cell, where the promoter is positioned to

CC provide for expression of a polynucleotide encoding a polypeptide from a

CC microbial source. The invention also relates to a transformed plant

CC comprising the recombinant DNA construct and a method of producing a

CC transformed plant having an improved property. The plant is a crop plant

CC such as maize or soybean. The method of producing a transformed plant

CC having an improved property comprises transforming a plant with the

CC recombinant DNA construct and growing the transformed plant, where the

CC polynucleotide or polypeptide is useful for improving plant properties.

CC The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,

CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,

CC increased resistance to plant disease, better growth rate by modification

CC of the cell cycle pathway with plant growth regulators, increased rate of

CC homologous recombination, modified seed oil or protein yield and/or

CC content, improved yield by modification of carbohydrate, nitrogen or

CC phosphorus use and/or uptake, by modification of photosynthesis or by

CC providing improved plant growth and development under at least one stress

CC condition, improved lignin production or improved galactomannan

CC production. This sequence represents a bacterial polypeptide used in the

CC scope of the invention. Note: The sequence data for this patent did not

CC form part of the printed specification but was obtained in electronic

CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX

XX Sequence 306 AA;

Query Match 34.7%; Score 535.5; DB 8; Length 306;

Best Local Similarity 38.5%; Pred. No. 1.5e-39;

Matches 115; Conservative 69; Mismatches 106; Indels 9; Gaps 4;

QY 4 LLELKNVSKTIRGKKIIEGLSPDVRAGEIFGFLGPNAGAKTTTIRMIVGHMSITAGEIAV 63

Db 7 LIETNNLTWYKHVAVDRINLKVKEGIYGLFPGNAGAKTTTIRMLLGLIKASHGSIKI 66

QY 64 CGVSVKENFEKAARHIGAIVENPELYKFLTGYQNIQQVARMYGVTKKIDELVELVGLK 123

Db 67 FGKDLKQHRLDILKNIGALVESPSYVPHLSGDNLETVRKIVK-VPKSRIAEVLVRLT 125

QY 124 NRINDKVTYSIGMRQRLGLAQSLHDPKLLILDEPTNGLDPAGIREIDYLRKLTREGK 183

Db 126 KVADRKVOEYSLGMKQRLAIAAALLANPRLVILDEPTNGLDPAGIREIDYLRKLTREGK 185

QY 184 MAVIVSSHLLSMELMCDRIATIQNGKLRDIOHVHGPARDEKKYVYIQADDTQALTREA 243

Db 186 ITVLLSSHLLSEVQVQSGVGIAGKLIQFQDSIELRKKANKRIFLSTSHPEV----AA 241

QY 244 AF---RKVKVDEAEGGIELSIQKD-EVPDLIKHLTDGVRVLYEVKAVNKSLSDRFUEIT 298

Db 242 TTLQERGINVDQARGLVWMDRSDEIAQLVKAFVEKIDIVYRISDETSSLEEIFLQLT 300

RESULT 9

ADN27185

ID ADN27185 standard; protein; 299 AA.

XX

XX AC ADN27185;

XX

XX 02-DEC-2004 (first entry)

XX

XX Bacterial polypeptide #9838.

XX

XX Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

KW pathogen tolerance; pest tolerance; plant disease resistance;

KW cell cycle pathway modification; plant growth regulator;

KW homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

KW bacterial polypeptide.

XX Bacteria.

OS US2003233675-A1.

XX

XX PN 18-DEC-2003.

XX

XX 20-FEB-2003; 2003US-00369493.

XX

XX 21-FEB-2002; 2002US-0360039P.

XX

XX (CAOY/) CAO Y.

XX (HINK/) HINKLE G J.

XX (SLAT/) SLATER S C.

XX (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

XX

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

PI WPI; 2004-061375/06.

XX

XX New recombinant DNA construct comprising a promoter positioned to provide

PT for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.

XX

XX Claim 1; SEQ ID NO 9838; 122pp; English.

XX

XX The invention relates to a recombinant DNA construct comprising a

CC promoter functional in a plant cell, where the promoter is positioned to

CC provide for expression of a polynucleotide encoding a polypeptide from a

CC microbial source, useful for producing plants with improved properties.

ADN46530
ID ADN46530 standard; protein; 309 AA.
XX
AC ADN46530;
XX
XX
DT 01-JUL-2004 (first entry)
XX
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID408.
XX
XX gene disruption; gene targeting; marker gene; transformation;
KW homologous recombination; hyperthermostable archaeobacterium; KOD1;
KW gene structure; gene function; enzyme activity; medicine;
KW forensic science; food; drug inspection; molecular biology; immunology.
XX
OS Thermococcus kodakaraensis.
XX
XX WO2004022736-A1.
PN
XX
XX 18-MAR-2004.
PD
XX
XX 29-AUG-2003; 2003WO-IB003597.
PF
XX
XX 30-AUG-2002; 2002JP-00319011.
PR
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA
XX Imanaka T, Atomi H;
PI
XX
DR WPI; 2004-257583/24.
XX
XX Method for disrupting targeted gene in genome of organism particularly
PT thermostable bacterium and with genome chips for analysis, applicable in
PT studying gene structure and functions.
PT
XX
XX Claim 9; SEQ ID NO 408; 598pp; Japanese.
PS
XX
XX This invention relates to a novel method for targeting disruption of an
CC arbitrary gene in a genome of an organism which comprises providing the
CC whole sequential data of the genome of such organism, selecting at least
CC 1 arbitrary region in the sequence, providing a vector that contains a
CC sequence homologous with the selected region and a marker gene,
CC transformation, and homologous recombination. The genome is preferably
CC the genome of a hyperthermostable archaeobacterium, particularly
CC Thermococcus kodakaraensis KOD1. The method is for targeting the
CC disruption of a gene in the genome of an organism, which is applicable in
CC studying gene structure and functions as well as enzyme activities of
CC encoded proteins and useful in medicine, forensic science, food or drug
CC inspection, molecular biology and immunology. With this method, the
CC disruption of a gene at an arbitrary position in a genome can be achieved
CC efficiently and reliably. The present sequence is that of a protein
CC encoded by the genome of Thermococcus kodakaraensis which was derived
CC using the method of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 309 AA;

Query Match 31.8%; Score 490; DB 8; Length 309;
Best Local Similarity 36.8%; Pred. No. 1.9e-35;
Matches 113; Conservative 70; Mismatches 108; Indels 16; Gaps 5;

QY 7 LKNVSTIRCKKIEGLSFDVRAGELFGFGPNAGKTTIRIMVGHMSITAGSIACVGV 66
DB 8 IENLTSYGTFRVADGTFDVKGEVFGFGPNAGKTTILSMGLIIPDDGRILGM 67
QY 67 SVKENFEKAARHICAIIVENPELYKFTGYQNLOQYA---BMTXGVTKKKIDIELVLGLK 123
DB 68 DMSREPIKIKERIGYLPENATIGELTAWKNLFFANFYRMSNSEREKRTITELKRVGLW 127
QY 124 NRINDKVTYSLGMRQRLGIAQSLHDPKLLILDEPTNGLDIPAGIEIRLYRLKLTREKG 193
DB 128 DARYRKAKTFSKGMKQRLLAQALINDPELLILDEPTSGLDLDPGALHVKVEVIRE-AKAE 196

QY 184 MAVIVSSHLSELMCDRIATIQNKLRDIOHVHGPARDKRYKRYIQADDTQALTREAA 243
DB 187 RTVFFSSHLSEVLSDRVGIIVRGLKAV---GPIR-EIKQFMELGEYIKVETKE 241
QY 244 AFRKVKVDE-----AEGGIELSQKDEVPDLIKHLTDGVRLYEVKAVNKLSLEDRFLE 296
DB 242 PIPELRHEITRVERLAPNRILFARSDIREWLSQYLTSGVTLTSLSEVEEPSLEDFVMK 301
QY 297 ITADKEE 303
DB 302 TIYGRDE 308

RESULT 15
ADS27537
ID ADS27537 standard; protein; 221 AA.
XX
AC ADS27537;
XX
XX 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #16570.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 16570; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of

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OM protein - protein search, using sw model

Run on: July 13, 2006, 13:44:12 ; Search time 40 Seconds
(without alignments)
738.464 Million cell updates/sec

Title: US-10-510-941-2
Perfect score: 1542
Sequence: 1 LETLLEKKNVSKTIRGKKII.....KSLDRFLEITADKEAQHV 307

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 80:*
1: Piri:*
2: Piri:*
3: Piri:*
4: Piri:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1027	66.6	305	2 D69822	ABC transporter (A
2	734	47.6	301	2 AD1169	ABC transporter (A
3	730	47.3	301	2 AF1526	Similar to ABC tra
4	680	44.1	312	2 G96916	ABC transporter, A
5	671.5	43.5	308	2 E69771	ABC transporter, A
6	667	43.3	318	2 H96917	ABC transporter, A
7	641	41.6	306	2 AD1642	ABC transporter (A
8	639	41.4	306	2 AD1279	ABC transporter (A
9	638	41.4	300	2 D97272	protein from GDSL
10	535.5	34.7	306	2 E83705	ABC transporter (A
11	528.5	34.3	242	2 B96935	ABC transporter, A
12	523	33.9	306	2 D97151	ABC transporter MD
13	515	33.4	306	2 S77627	bacitracin transpo
14	512	33.2	306	2 T31682	bcrA protein - Bac
15	504.5	32.7	299	2 T09008	probable ATP-bind
16	493	32.0	308	2 H71008	probable ATP-bind
17	491.5	31.9	318	2 C71197	ABC transporter (A
18	486	31.5	307	2 H83705	ABC transporter (A
19	484	31.4	301	2 JCS348	cdd4 protein - Clo
20	475	30.8	314	2 D97318	ABC-type MDR trans
21	473	30.7	305	2 E75122	hypothetical prote
22	471	30.5	314	2 B83752	bacitracin ABC tra
23	464	30.1	311	2 G69803	ABC transporter (A
24	463.5	30.1	294	2 G69391	ABC transporter, A
25	463.5	30.1	312	2 G97260	ABC-type MDR trans
26	461.5	29.9	313	2 G97006	ABC-type multidrug
27	451.5	29.3	318	2 H75157	daunorubicin resis
28	450	29.2	307	2 B97006	ABC-type multidrug
29	444.5	28.8	312	2 T29454	ABC transport prot

transposase (08) /
ABC transporter AT
ABC transporter AT
ABC transporter, A
spaf protein - Bac
ABC transporter (A
ABC transporter (A
ABC transporter (A
gliding motility p
ABC transporter (A
hypothetical prote
ABC transporter (A
probable ABC-type
ABC transporter (A
probable ATP-bind

ALIGNMENTS

RESULT 1

D69822

ABC transporter (ATP-binding protein) homolog yhcH - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004

C;Accession: D69822

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holstappel, S.; Hosono, S.; Hullo, M.F

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinol

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue

V., M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowaka, A.; Sero

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,

A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: D69822

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-305 <KUN>

A;Cross-references: UNIPROT:P54592; UNIPARC:UPI0000060122; GB:Z99108; GB:AL009126; NID

A;Experimental source: strain 168

C;Genetics:

A;Gene: yhcH

C;Keywords: ATP; nucleotide binding; P-loop

F;20-209/Domain: ATP-binding cassette homology <ABC>

F;37-44/Region: nucleotide-binding motif A (P-loop)

Query Match 56.6%; Score 1027; DB 2; Length 305;

Best Local Similarity 65.1%; Pred. No. 1.3e-57;

Matches 200; Conservative 47; Mismatches 56; Indels 4; Gaps 2;

QY 1 LETLLEKKNVSKTIRGKKIIIEGLSFVDRAGEIFGFLGPNAGKTKTTIRMTVGHMSITAGE 60

Db 1 MKTVLEKKNVKNIRGRTIIDLSTFIREGEVFGFLGPNAGKTKTTIRMMVGLMKLSKGD 60

QY 61 IAVGVSVKENFKAARHGAIVENPELYKFLTGYNLQYARMTKGVTKKKIDIEIVELY 120

Db 61 VLICGQSITKEVAKAIKHGAIVENPELYKFLSGYKNLQGFARMVKGVTKEKIDIVEVELV 120

QY 121 GLKNRINDKVTYSLGMRQELGLAQSLLHDPKLLIIDEPTNGLDPPAGIRIRYLKLT 180

Db 121 GLTDRIHDKVTYSLGMRQELGLAQSLLHDPKLLIIDEPTNGLDPPAGIRIRYDLKLT 180

QY 181 EKGMAIVSVSHLLSELMELMCDRIAITQNGKLRDIQHVHGPARDEKKRYVIAQADDTQALTR 240

Db 181 ERGMVIVSSHLLSEMELMCDRIAILQKGLIDIQNVKDNIDENDTYFFQVEQP---SE 237

Qy 241 EAAAFKVKVDKAEAGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLDRFLRLEITAD 300

Db 238 AATVLYNOYDLSKTNVGEVYKLAKEEVPVAVIELLMQOIRIYEVKVIKTSLEDRFLEMTGE 297

Qy 301 -KEEAQH 306

Db 298 TKEEVQH 304

RESULT 2

ABC transporter (ATP-binding protein) lmc0756 [imported] - Listeria monocytogenes (strain AD1169

C;Species: Listeria monocytogenes

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004

C;Accession: AD1169

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Feihl, H.; D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makok, C.; Schluetter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative Genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AD1169

A;Status: preliminary

A;Molecule type: DNA

A;Query Match 47.6%; Score 734; DB 2; Length 301;

A;Best Local Similarity 49.8%; Pred. No. 3.5e-39;

A;Matches 149; Conservative 61; Mismatches 81; Indels 8; Gaps 3;

Qy 2 ETTLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSITAGEI 61

Db 3 ERALQVNLHKKIRKREIIKIGISFVPGVEFGLGPNAGAGKTTTIRMIVGLIKPSTGTI 62

Qy 62 AVCGSVKKNFEKAARHIGAIVNPELYKLTGYQNLOQYARMTKGVTKKKIDIEIVELVG 121

Db 63 LIGGKDIRKNFTAMRGLSGSIVENPEFYTLTGQENLAYFARMDSIKKERIQEVTELVG 122

Qy 122 LKNRINDKVYTSLSGMRQRLGLAQSLLHDPKLLILDEPTNGLDPPAGIREIRDYLRKLTRE 181

Db 123 LEKRIINDRVSTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPPSGIHEMRDFIRALARN 182

Qy 182 KGMVIVSSHLLSEMELMCDRIAILQNGK-LRDIQHVHGPARDKKRYVIOADDTQALTR 240

Db 183 EGISVLSSHLLSEIELLCRDVAIMTDGTIIKTQVSHLLSSRAQLRWLTPPEQA-----IE 236

Qy 241 EAAAF-RKVKVDKAEAGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLDRFLRLEIT 298

Db 237 QAKAFLESVTEVEVDGVLVTAMNEESAENWELVAKGIKVHIDKRRKPSLEDLFLELT 295

RESULT 3

AF1526

Similar to ABC transporter (ATP-binding protein) lin0750 [imported] - Listeria innocua

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004

C;Accession: AF1526

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Feihl, H.; D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makok, C.; Schluetter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative Genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AF1526

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-301 <GLA>

A;Cross-references: UNIPROT:Q92DR3; UNIPARC:UPI000000CC33A; GB:AL592022; PIDN:CAC95982.1

A;Experimental source: strain Clip11262

C;Genetics:

A;Gene: lin0750

Query Match 47.3%; Score 730; DB 2; Length 301;

Best Local Similarity 49.5%; Pred. No. 6.2e-39;

Matches 147; Conservative 57; Mismatches 89; Indels 4; Gaps 1;

Qy 2 ETTLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSITAGEI 61

Db 3 ELALQVNLHKKIRKREIIKIGISFVPGVEFGLGPNAGAGKTTTIRMIVGLIKPSTGTI 62

Qy 62 AVCGSVKKNFEKAARHIGAIVNPELYKLTGYQNLOQYARMTKGVTKKKIDIEIVELVG 121

Db 63 LIGGKDIRKNFTAMRGLSGSIVENPEFYTLTGQENLAYFARMDSIKKERIQEVTELVG 122

Qy 122 LKNRINDKVYTSLSGMRQRLGLAQSLLHDPKLLILDEPTNGLDPPAGIREIRDYLRKLTRE 181

Db 123 LEKRIINDRVSTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPPSGIHEMRDFIRALARN 182

Qy 182 KGMVIVSSHLLSEMELMCDRIAILQNGKLRDIQHVHGPARDKKRYVIOADDTQALTR 241

Db 183 EGISVLSSHLLSEIELLCRDVAIMTDGTIIKTQVSHLLSSRAQLRWLTPPEQA----- 238

Qy 242 AAFKVKVDKAEAGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLDRFLRLEIT 298

Db 239 KAFASVTEVEVDGVLVTAVNERSAENWELVAKGIQVHIDKRRKPSLEDLFLELT 295

RESULT 4

G96916

ABC transporter, ATP-binding component CAC0138 [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004

C;Accession: G96916

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: G96916

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-312 <KUR>

A;Cross-references: UNIPROT:Q97M04; UNIPARC:UPI000000C9D83; GB:AB001437; PIDN:NAK78122.1

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC0138

Query Match 44.1%; Score 680; DB 2; Length 312;

Best Local Similarity 46.0%; Pred. No. 9e-36;

Matches 139; Conservative 60; Mismatches 101; Indels 2; Gaps 2;

Qy 4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSITAGEI 63

Db 4 VLEKVDKVKHIGKREIIKIGISFVPGVEFGLGPNAGAGKTTTIRMIVGLIKPNSGSIKI 63

Qy 64 CGVSVKKNFEKAARHIGAIVNPELYKLTGYQNLOQYARMTKGVTKKKIDIEIVELVGLK 123

Db 64 MGHDIQEKELKSNVGCIVENPDWYGLTGRENLIQYAKWYGSVSKERIDEVAEIIIGLK 123

Qy 124 NRINDKVYTSLSGMRQRLGLAQSLLHDPKLLILDEPTNGLDPPAGIREIRDYLRKLTREK 183

Db 124 DRINDKVYTSLSGMRQRLGLAQSLLHDPKLLILDEPTNGLDPPGIMDFRIVRLMAENK 183

Qy 184 MAVIVSSHLLSEMELMCDRIAILQNGKLRDIQHV-HGPARDKKRYVIOADDTQALTR 242

Db 184 SAVFISHLIAEQVCDTVAFINGGEIKSEKSEKGTENFGIATSNINLAMETL 243

```

Qy 243 AAFKRV-KVDEARGGIELSIQKQVDPDLIKHLTSGVRLYEVKAVNKSLEDRFLFEITADK 301
Db 244 SKLPFVYEVKNNEDKISAAIQGYSPKVIABLMKNSVEVIEFYKHKHTLEDRFMQIVEGE 303
Qy 302 EE 303
Db 304 EE 305

RESULT 5
B69771
ABC transporter (ATP-binding protein) homolog ydbJ - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C:Accession: B69771
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertone, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chodura, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallenbach, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.; Koetter, P.; Koningsstein, G.; Kroch, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauelet, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetellelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot, A.; Teuch, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, K.; T. Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: B69771
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-308 <KUN>
A:Cross-references: UNIPROT:P96605; UNIPARC:UPI000005FF63; GB:Z99106; GB:AL009126; NID:G
A:Experimental source: strain 168
C:Genetics:
A:Gene: ydbJ
C:Keywords: ATP; nucleotide binding; P-loop
F:21-210/Domain: ATP-binding cassette homology <ABC>
F:38-45/Region: nucleotide-binding motif A (P-loop)

```

Query Match	43.5%	Score	671.5	DB 2	Length	308			
Best Local Similarity	42.7%	Pred. No.	3.1e-35						
Matches	131	Conservative	71	Mismatches	102	Indels	3	Gaps	2

Qy	2	ETLLELKNVSKTIRGKKII	EGLSFDVRAGEIF	FGFLGPNAGACKTTIR	MIIVCHMSITAGEI	61
		:::	:::	:::	:::	:::
Db	3	EPILHIEGLDKKIGSKQIL	KQISMDVMEGELIGL	GPNGSGKTLIRII	VGLLKKQNSGV	62
		:::	:::	:::	:::	:::
Qy	62	AVCCVSVKENPEKAA	RHIGAIVENPELYK	FLTGYQNLQOVARMTK	GVTKKIDIVEIVLG	121
		:::	:::	:::	:::	:::
Db	63	TISGFQHDTEFEKA	WEAAGAIVENPEFY	LYTGWENLKFHANM	HKKIADERLDEV	122
		:::	:::	:::	:::	:::
Qy	122	LKNRINDKVITYSL	IGMQRGLAQSLHD	PKLLILDSEPTNGLD	PAGIREINDYLRKLTRE	181
		:::	:::	:::	:::	:::
Db	123	LTSAIHDKVITYSL	IGMQRGLGIAQAIL	HRPKLLILDSEPTNGLD	PAGMKQFRDHIKELAE	182
		:::	:::	:::	:::	:::
Qy	182	KGMAVIVSSHLS	EMELMCDRIATION	GKLARDIOHVHGPAR	DEKRYIYIQANDTQAL	241
		:::	:::	:::	:::	:::
Db	183	EGTAVLPATHLL	REVDELCDRVIIIG	KEIKAEVSLQGTQDTT	EKAIEVQPOEKANWL	242
		:::	:::	:::	:::	:::
Qy	242	AAAFRKVKVDEA	EGGIELSKQDEVP	DLIKHLTDSGVRLYE	VKAVNKSLEDRFLE-ITAD	300
		:::	:::	:::	:::	:::
Db	243	TG--NQYQAESQ	DGTIVVEAKENI	PELNSRLVQCDL	NVPSITPYTQTSLE	DEFIKATTAH 300
		:::	:::	:::	:::	:::
Qy	301	KEEAQHV	307			
		:::				
Db	301	QEEGEEL	307			
		:::				

RESULT 6

H96917
ABC transporter, ATP-binding protein CAC0147 [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004
C/Accession: H96917
E;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H96917
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-318 <KUR>
A;Cross-references: UNIPROT:Q97WPS; UNIPARC:UPI00000CC9D8B; GB:AE001437; PIDN:AAK78131.1
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0147

Query Match 43.3%; Score 667; DB 2; Length 318;
Best Local Similarity 42.9%; Pred. No. 6.1e-35;
Matches 133; Conservative 69; Mismatches 92; Indels 16; Gaps 4;

Qy 1 LETLLEKNVSKTRIGKKIIEGSLFVDVRAGEIFGLFGNGAGKTITRMIVGHMSITAGE 60
Db : ::
1 MSNVLEVTDLYKKLGKNEKIIGISFSIKGEIILFLGRNGAGKTTTAKMLVGLITPDKGS 60

Qy 61 IAVCGSVKENFEKAARHGAIVENPELYKFTCYQNLOQYARMTKGVTKKIDIVELV 120
Db : ::
61 VMISGHDDITKEASEALSCVGAIVENPELYSYLTQRNLQEOVARFYKOITKEDIKIGNTV 120

Qy 121 GLKNRINDVKYTSGLNRQRLGLAOSLLHPDKLLILDPTNGLDPAGIREIRDYLRKLTR 180
Db : ::
121 GLSRLDEKVKYSGLGNKQRLGLAELISPKLLILDPTNGLDPTGLIIERNLLKKOAK 180

Qy 181 EKGMAVTSSHLSEMBELCMCDRIATIQNGKLRDIQHVGPARDEKKRYITQADDTQALTR 240
Db : ::
181 ENKMAIFVSSHILSETIQLCORVAFIGGIKSFKETLKGTNKDHKTESF---ENVMIMTK 237

Qy 241 E----AAAFPRVK-----VDAEG--GIELSIQKDEVPDLKHLTDSGVRLVEYKAVN 287
Db : ::
238 EKDKCTEALKEIGFIIDFKLADESNGIYTTFEAKAKLDSVPDITSSLAEEKIRIEQIYKRQ 297

Qy 288 KSLEDREFLEI 297
Db 298 QNLEDRIYEL 307

RESULT 7

AD1642
ABC transporter (ATP-binding protein) homolog lin1677 [imported] - Listeria innocua (st
C/Species: Listeria innocua
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C/Accession: AD1642
R;Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; I
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant
A;Title: Comparative Genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1642
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-306 <GLA>
A;Cross-references: UNIPROT:Q92B73; UNIPARC:UPI00000CC61A; GB:AL592022; PIDN:CAC96908.1
A;Experimental source: strain Clpl11262
C;Genetics:
A;Gene: lin1677

Query Match 41.6%; Score 641; DB 2; Length 306;

Db 67 FGDKLQKRLDILKNIGALVESPSYPHLSGEDNLETVRKIVK-VPKSRIAELVRLT 125
Qy 124 NRINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAIGREIRDLVRLTREKG 183
Db 126 KVADRKQVETSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAIGREIRDLVRLTREKG 185
Qy 184 MAVIVSHLLSELMCDRIATIIQNGKLRDIOHVHGPARDKKRYIIQADDTQALTRAA 243
Db 186 ITVLSSHLLSEVQASQVGIAGKLIQFDSIEELRKANRKFILSTSHPEV---AA 241
Qy 244 AF---RKVKVDEAGGIELSTQKD-EVPDLIKHITDSGRLYEYKAVNKSLDEPLEIT 298
Db 242 TILOERGINVDQTARGLVMNDRSDEETAAQLVKAPEKIDIVYRISDETSSLEEFLOLT 300
RESULT 11
B96935
ABC transporter, ATP-binding protein CAC0288 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 31-Dec-2004
C;Accession: B96935
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B96935
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-242 <KUR>
A;Cross-references: UNIPROT:Q97WB0; UNIPARC:UPI000000C9DFE; GB:AE001437; PIDN:AAK78269.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0288

Query Match 34.3%; Score 528.5; DB 2; Length 242;
Best Local Similarity 48.6%; Pred. No. 2.3e-26;
Matches 101; Conservative 49; Mismatches 57; Indels 1; Gaps 1;
Qy 4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGE 63
Db 5 VVEINLSKTYRGFNNAVNNINLIREGRIVYGLGPNAGKSTTIRMILGLIKNSSGSIKI 64
Qy 64 CGSVKVENFEKAARHIGAIVENPELYKFLTGYNLQOYARMYKGVTKKKIDEIVELVGLK 123
Db 65 FGKLNKENRAEILKNGVALVESPSYGHNLNAYENLKIWSYI-KGVDKNAIDEVLKLVNLY 123
Qy 124 NRINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAIGREIRDLVRLTREKG 183
Db 124 EHRKKVSKFSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAIGREIRDLVRLTREKG 183
Qy 184 MAVIVSHLLSELMCDRIATIIQNGKLRDIOHVHGPARDKKRYIIQADDTQALTRAA 211
Db 184 KTIISHSILSELMCDRIATIIQNGKLRDIOHVHGPARDKKRYIIQADDTQALTRAA 211

RESULT 12
D97151
ABC transporter MDR-type, ATPase component CAC2040 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004
C;Accession: D97151
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D97151
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-306 <KUR>
A;Cross-references: UNIPROT:Q97HH1; UNIPARC:UPI000000CA3C9; GB:AE001437; PIDN:AAK79999.1;
A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:
A;Gene: CAC2040
Query Match 33.9%; Score 523; DB 2; Length 306;
Best Local Similarity 39.5%; Pred. No. 6.6e-26;
Matches 121; Conservative 65; Mismatches 106; Indels 14; Gaps 6;
Qy 1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGE 60
Db 1 MKYLVRFTNLTKKYKNTSVVENLNIEQOYIYGLGPNAGKTTTIRMILGLMKISTGE 60
Qy 61 IAVCGSVKENFEKAARHIGAIVENPELYKFLTGYNLQOYARMYKGVTKKKIDEIVELV 120
Db 61 VELFG--EKNPRTSIYKKIGSIIEYPGFYNLTAEENLDIHRMMKIENQKXINETLTMV 118
Qy 121 GL-KNRI-NDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAIGREIRDLVRL 178
Db 119 GLDSNISKVKKNFSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAIGREIRDLVRL 178
Qy 179 TREKGMVIVSSHLLSELMCDRIATIIQNGKLRDIOHVHGPARDKKRYIIQADDTQAL 238
Db 179 CKDGRITLVSSHLLSELMCDRIATIIQNGKLRDIOHVHGPARDKKRYIIQADDTQAL 234
Qy 239 TREAAAPRK---VKVDEAEG--GIELSIOKDEVPDLIKHITDSGRLYEYKAVNKSLDE 292
Db 235 VKEACSLIKNNLAIKDYIELIGDAIKYKINESSTIAKTLIKNDIELYEMSFSDNLED 294
Qy 293 RFLIEIT 298
Db 295 YFVKVT 300
RESULT 13
S77627
bacitracin transport protein bcrA - Bacillus licheniformis
C;Species: Bacillus licheniformis
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 05-Oct-2004
C;Accession: S77627
R;Podlessek, Z.; Comino, A.; Herzog-Velikonja, B.; Zgur-Bertok, D.; Komel, R.; Grabnar, M.; Mol. Microbiol. 16, 969-976, 1995
A;Title: Bacillus licheniformis bacitracin-resistance ABC transporter: relationship to
A;Reference number: S77627; MUID:96059642; PMID:7476193
A;Accession: S77627
A;Molecule type: DNA
A;Residues: 1-306 <POD>
A;Cross-references: UNIPROT:P42332; UNIPARC:UPI0000126845; EMBL:L20573; NID:9466477; PI
A;Experimental source: strain ATCC 9945A
C;Genetics:
A;Gene: bcrA
A;Start codon: TTG
C;Keywords: antibiotic resistance; ATP binding; nucleotide binding; P-loop
F;20-209/Domain: ATP-binding cassette homology <ABC>
F;37-44/Region: nucleotide-binding motif A (P-loop)

Query Match 33.4%; Score 515; DB 2; Length 306;
Best Local Similarity 36.6%; Pred. No. 2.1e-25;
Matches 113; Conservative 76; Mismatches 98; Indels 22; Gaps 5;
Qy 1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGE 60
Db 1 MSTIITKTDLTLMYKQSKSVHDHINVKQDIYVGLGRNAGKTTTIRMILGLIKPTSGQ 60
Qy 61 IAVCGSVKENFEKAARHIGAIVENPELYKFLTGYNLQOYARMYKGVTKKKIDEIVEL 119
Db 61 IEIFGFENFPKCKEILLRIGSIIEVPGFYANLTARENLLINAKII-GIHKNAIDEVLEI 119
Qy 120 VGLKNRINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAIGREIRDLVRL 179
Db 120 VGLQHEHTKVLGKFSGLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAIGREIRDLVRL 179
Qy 180 REKGMVIVSSHLLSELMCDRIATIIQNGKLRDIOHVHGPARDKKRYIIQADDTQAL 238
Db 180 KERNITIFISSHLLSELMCDRIATIIQNGKLRDIOHVHGPARDKKRYIIQADDTQAL 239

QY 239 TREAAAFKVKVDEAEGGIELSIQKDEVPDLIKHL-----TDSGVRLYEVKAVNK 288
 Db 240 -----VLMQHFHDHDEYHQDGIIRVYSHLQOQKLNKLFVENGIDVLKITMSD 290
 QY 289 SLEDRFLEI 297
 Db 291 SLEDYFVKL 299

RESULT 14
 T31682
 bcra protein - Bacillus licheniformis
 C:Species: Bacillus licheniformis
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 05-Oct-2004
 C:Accession: T31682
 R:Kenz, D.; Klens, A.; Schorgendorfer, K.; Marahiel, M.A.
 Chem. Biol. 4, 927-937, 1997
 A:Title: The bacitracin biosynthesis operon of Bacillus licheniformis ATCC 10716: molecu
 A:Reference number: 221058; MUID:98089193; PMID:9427658
 A:Accession: T31682
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-306 <CON>
 A:Cross-references: UNIPROT:Q9SSV9; UNIPARC:UPI00000AF215; EMBL:AF007865; NID:94464275;
 C:Genetics:
 A:Gene: bcra

Query Match 33.2%; Score 512; DB 2; Length 306;
 Best Local Similarity 36.2%; Pred. No. 3.3e-25;
 Matches 112; Conservative 76; Mismatches 99; Indels 22; Gaps 5;

QY 1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGAGTKTTIRMIVGHMSITAGE 60
 Db 1 MSTIIITDITKMYGSKQSDHNLNINVKQDIIYVGLRNGAGTKTTIRMLLGLIKETSGQ 60
 QY 61 IAVCGSVSKENFEKAARHIGAIIVENPELYKFLTYGYNLQOYARMTKGVTKK-IDBIVEL 119
 Db 61 IEIFGENFFKNKEILLRIGSIVVEVGFYANLTARENLLINAKII-GIHKNAIDVLEI 119
 QY 120 VGLKNRINDKVTYSGLMRQRLGLAOSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKL 179
 Db 120 VGLQHETKVLGVKFLSGMKQRLGARALLHYPSELSILDEPTNGLDPIGKEMERLIHSLA 179
 QY 180 REKGMVIVSSHLSEMLMCDRIATIIQNGK-LRDQHVHGPARDKRYIIOADDTQAL 238
 Db 180 KERNITFISHSILSETEQVHDVHGIHEGKLEELPFDFHLKRNKYLEFQLSDQNKAV 239
 QY 239 TREAAAFKVKVDEAEGGIELSIQKDEVPDLIKHL-----TDSGVRLYEVKAVNK 288
 Db 240 -----VLMQHFHDHDEYHQDGIIRVYSHLQOQKLNKLFVENGIDVLKITMSD 290
 QY 289 SLEDRFLEI 297
 Db 291 SLEDYFVKL 299

RESULT 15
 T09008
 cdd4-like protein ScnF - Streptococcus pyogenes
 C:Species: Streptococcus pyogenes
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 05-Oct-2004
 C:Accession: T09008
 R:Hynes, W.L.; Ferretti, J.J.; Tagg, J.R.
 Appl. Environ. Microbiol. 59, 1963-1971, 1993
 A:Title: Cloning of the gene encoding streptococcal A-Ff22, a novel lantibiotic produced
 A:Reference number: A58598; MUID:93319301; PMID:8328813
 A:Accession: T09008
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-299 <HYN>
 A:Cross-references: UNIPROT:O31054; UNIPARC:UPI00000B5C5D; EMBL:AF026542; NID:92502065;
 A:Experimental source: strain Ff22

C:Genetics:
 A:Gene: scnF
 C:Keywords: antibiotic biosynthesis
 F:20-209/Domain: ATP-binding cassette homology <ABC>

Query Match 32.7%; Score 504.5; DB 2; Length 299;
 Best Local Similarity 39.4%; Pred. No. 9.4e-25;
 Matches 121; Conservative 59; Mismatches 102; Indels 25; Gaps 6;

QY 1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGAGTKTTIRMIVGHMSITAGE 60
 Db 1 MKNAIELKLSKVQDITTVDEKLTIVREGEIYGLGPNAGAGTKTTMKWILSLVSPTLGE 60
 QY 61 IAVCGSVSKENFEKAARHIGAIIVENPELYKFLTYGYNLQOYARMTKGVTKKIDIEIVELV 120
 Db 61 ILINGEDIKGN-HAYLRVIGSMIEEPSYVPLNTGYENLLVFQKMW-GPDESNIWPTLALV 118
 QY 121 GLKNRINDK--VKTYSGLMRQRLGLAOSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKL 178
 Db 119 GLAENNRKLVKAYSLGMKQRLGARALLHYPSELSILDEPTNGLDPIGKHEIRELIVKL 178
 QY 179 TREKGMVIVSSHLSEMLMCDRIATIIQNGK---RDQHVHGPARDKRYIIOADDT 235
 Db 179 AKERGLTWFISQIILSEIEHIAIRVGIINHGRLVVEGEIEAIKSNWTWIEIGDFFSQNNIV 238
 QY 236 QALTR-----EAAAFKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVN 287
 Db 239 QSLINVQVEVLGASASHVKFK-----NIDNDKLADVGTILIENDYRIFRYVRES 288
 QY 288 KSLDRP 294
 Db 289 ENLEDIF 295

Search completed: July 13, 2006, 13:49:44
 Job time : 41 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model
Run on: July 13, 2006, 13:40:51 ; Search time 298 Seconds
(without alignments)
952.952 Million cell updates/sec

Title: US-10-510-941-2
Perfect score: 1542
Sequence: 1 LETLLEKNVSKTIRGKKII.....KSLDRFLEITADKERAQHV 307

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1540	99.9	307	2	Q65M37 bacillus li
2	1027	66.6	305	1	P54592 bacillus su
3	806	52.3	307	2	Q8EQI5 OCEIH
4	789	51.2	300	2	Q6H1J7 BACAN
5	789	51.2	300	2	Q6H1J0 BACHK
6	785	50.9	300	2	Q4MSI3 BACCCE
7	785	50.9	300	2	Q73BE3 BACC1
8	784	50.8	300	2	Q3EML1 BACTI
9	783	50.8	300	2	Q63E15 BACCZ
10	781	50.6	300	2	Q81G51 BACCR
11	754.5	48.9	305	2	Q6HAN5 BACHK
12	748.5	48.5	305	2	Q81JQ2 BACAN
13	744.5	48.3	305	2	Q3EW61 BACTI
14	743.5	48.2	305	2	Q72X49 BACC1
15	739.5	48.0	305	2	Q4MLR2 BACCCE
16	739.5	48.0	305	2	Q814M7 BACCR
17	738	47.9	306	2	Q81AB3 BACC1
18	735.5	47.7	305	2	Q63OK0 BACCZ
19	734	47.6	301	2	Q8Y8V6 LISTERIA
20	733	47.5	311	2	Q6HFD4 BACHK
21	733	47.5	311	2	Q733F8 BACC1
22	731	47.4	320	2	Q4MNN2 BACCCE
23	730	47.3	301	2	Q92DR3 LISTERIA
24	728	47.2	301	2	Q4EUC2 LISTERIA
25	728	47.2	331	2	Q637G1 BACCZ
26	727	47.1	301	2	Q4ELV1 LISMO
27	727	47.1	301	2	Q722F3 LISMF
28	712	46.2	304	2	Q5K2F8 GEOKA
29	709	46.0	268	2	Q81T80 BACAN
30	680	44.1	312	2	Q97MQ4 CLOAB
31	672	43.6	306	2	Q41AX1_9BACI

32	671.5	43.5	308	2	P96605 BACSU
33	670	43.5	304	2	Q2WL76_CLOBE
34	667	43.3	318	2	Q97MP5_CLOBE
35	666.5	43.2	307	2	Q5W112_BACSK
36	663	43.0	308	2	Q65N71_BACLD
37	660.5	42.8	319	2	Q81CN4_BACCR
38	658.5	42.7	303	2	Q895C2_CLOTE
39	641	41.6	306	2	Q92B73_LISIN
40	639	41.4	306	2	Q4EMV3_LISMO
41	638	41.4	306	2	Q8Y6P8_LISMO
42	638	41.4	300	2	Q65DD4_BACLD
43	638	41.4	300	2	Q97ET0_CLOAB
44	638	41.4	306	2	Q4EEG7_LISMO
45	638	41.4	306	2	Q71232_LISMF

ALIGNMENTS

RESULT 1
Q65M37_BACLD PRELIMINARY; PRT; 307 AA.
AC Q65M37; Q62XH4;
DT 25-OCT-2004, integrated into UniprotKB/TREMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE YHCH (ABC transporter).
GN Name=yhch; OrderedLocNames=BL03183, BL100969,
OS Bacillus licheniformis (strain DSM 13 / ATCC 14580).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=1538718; DOI=10.1159/000079829;
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baumeister S., Henne A., Liesegang H., Merkl R.,
RA Ehrenreich A., Gottschalk G.
RT "The complete genome sequence of Bacillus licheniformis DSM13, an
organism with great industrial potential."
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15461803; DOI=10.1186/gb-2004-5-10-r77;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA Tang M., Lopez de Leon A., Xiang H., Gusti V., Clausen I.G.,
RA Olsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,
RA Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N.,
RA Ehrlich S.D., Berk R.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus
licheniformis and comparisons with closely related Bacillus species."
RL Genome Biol. 5:RESEARCH077.1-RESEARCH077.12(2004).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
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CC -----
DR ENBL; A8017333; AAU39877.1; -; Genomic DNA.
DR ENBL; CP000002; AAU22534.1; -; Genomic DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0001666; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transp; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.
SQ SEQUENCE 307 AA; 34448 MW; A7ABD87C38EBFABA CRC64;

Query Match 99.9%; Score 1540; DB 2; Length 307;

[illegible]

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
NCBI_TaxID=1392;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Sterne;
RA Brettn T.S., Bruce D., Challacombe J.P., Gilna P., Han C., Hill K.,
RH Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RT Richardson P., Rubin E., Tice H.;
RL "Complete genome sequence of Bacillus anthracis Sterne";
RM Submitted (JAN-2004) to the EMBL/GenBank/DDJB databases.
CC - SIMILARITY: Belongs to the ABC transporter family.

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EMBL: AE017225; AAT53594.1; -: Genomic_DNA.
DR GO: G0:0005524; F: ATP binding; IEA.
DR GO: G0:0016887; F: ATPase activity; IEA.
DR GO: G0:0000166; F: nucleotide binding; IEA.
GO: G0:0006810; P: transport; IEA.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transp_like.
DR Pfam: PF00005; ABC_tran; 1.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER_1; UNKOWN_1.
DR PROSITE: PSS0893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Nucleotide-binding; Transport.
XQ
SQ SEQUENCE 300 AA; 33378 MW; 4FBIA80D719ACD92 CRC64;
Query Match 51.2%; Score 789; DB 2; Length 300;
Best Local Similarity 53.7%; Pred. No. 1.5e+36;
Matches 160; Conservative 59; Mismatches 69; Indels 10; Gaps 4;
Yq 4 LLEKNVSKTKIRKKIIEGLSPDVRAGEIPGFLPGNAGKTTHMIVGHMSITAGEIAV 63 ::: :: :: :: :: :: :: :: :: :: :: :
Db 5 VVKLENVRNKIGGTGIETRGLSPEFVEGVGFPLGNPSGGTTRTMWTGLISMTGEDITI 64 ::: :: :: :: :: :: :: :: :: :: :
Yq 64 CGVSVENPEKAARHGTAIVENPELYKFVTGYQNLOOAYAMT-KGVTKKKIDEIVELVL 122 ::: :: :: :: :: :: :: :: :: :: :
Db 65 CGHSITEREAKALEIQGAIVENPELDYDTGMQLKHFNMAITPISEKRIASIVKLVEL 124 ::: :: :: :: :: :: :: :: :: :: :
Yq 123 KNRRINDKVTSYLSGRQRCLQAQLSLHPDKLLILDPTNGLDPAIREIRDYLKLTREK 182 ::: :: :: :: :: :: :: :: :: :: :
Db 125 EHAIHKVVTSYGMRQLGIALHQPKILLDEPTNLGLDPAGIRIEDYLORLAKEE 184 ::: :: :: :: :: :: :: :: :: :: :
Yq 183 GMAVTVSSHLSEMMLWCRIAIIQNGKLRDIQHVGPAR-DCKKYRYIOADTOALTRE 241 ::: :: :: :: :: :: :: :: :: :: :
Db 185 NIATIVSSHLSELMLCDRWVIIKQGFEQYNLHEQAKHDFTVVVAPEVDQVQKA--- 241 ::: :: :: :: :: :: :: :: :: :: :
Yq 242 AAAPFRKVVDAREGG-IELS IQXEDVPDLKLHLTDSGLRVLEYKANXSLEDREFLEIT 298 ::: :: :: :: :: :: :: :: :: :: :
Db 242 ----NEIVOAGAOGNVIVSVTKBEIPQLVKLVNNDDVLVYGVTVQNTKLEDEF LAIT 295 ::: :: :: :: :: :: :: :: :: :: :
RESULT 5
O6HLJU_BACHK PRELIMINARY; PRt; 300 AA.
ID O6HLJU_BACHK AC O6HLJO;
DC 19-JUL-2004, integrated into UniprotKB/TreMBL.
DT DT 07-FEB-2006, entry version 14.
DE ABc transporter, ATP-binding protein; possible multidrug transporter.
CN Name=bctr; Ordered locus Names=B7927.1246;
OS Bacillus thuringiensis subspecies konkukian.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus;
OX Bacillus cereus group.
NB NCBI_TaxID=180856;
[1]
NP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=97-27;
RA Brettn T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,

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RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ABC transporter family.
CC -----
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CC -----
DR EMBL; A0017355; AAT59400.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.
SQ SEQUENCE 300 AA; 33378 MW; 4F8A80D719ACD92 CRC64;

Query Match 51.2%; Score 789; DB 2; Length 300;
Best Local Similarity 53.7%; Pred. No. 1.5e-36;
Matches 160; Conservative 59; Mismatches 69; Indels 10; Gaps 4;

QY 4 LLEKNVSTIRKGIIEGLSPDVRAGEIFGFLGPNAGKTTTIRMIVGHMSTAGEIAV 63
DB 5 VVKLENVRKIKGTEIIRGLSFVEVGEVYGLGPNAGKTTTIRMIVGHMSTAGEIAV 64
QY 64 CGVSVKENPEKAAHIGAIVENPELYKFLTYGNLQOYARMT-KGYTKKKIDIEIVLVL 122
DB 65 CGHSIRTEREKALEQIGAIVENPELYDYMTGMQNLKHPANMAITPISKERIAIIVKLVEL 124
QY 123 KNRINDKVTYSYSLGMRQRLGSLHDPKLLILDEPTNGLDPAGIREIDYLRKLTREK 182
DB 125 EHAHKKVKVTSYSLGMRQRLGSLHDPKLLILDEPTNGLDPAGIREIDYLRKLTREK 184
QY 183 GMAVIVSSHLLSEMLMCDRIALIQNGKLRIQHVHGPAR-DEKKRYYYQADDTQALTRE 241
DB 185 NIATIVSSHLLSEMLMCDRIALIQNGKLRIQHVHGPAR-DEKKRYYYQADDTQALTRE 241
QY 242 AAARFKVKVDEAGG-IEISIQKDEVDPLIKHLTDSGVRLYEYKAVNKSLDEDFLEIT 298
DB 242 ----NEIVQKGAQNVIVSVTKKEIPQLVKLVNNDVLVYGVTVQNKLTLEDEFLAIT 295

RESULT 6
Q4MSI3_BACCE PRELIMINARY; PRT; 300 AA.
AC Q4MSI3_
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Bacitracin transport ATP-binding protein bcrA.
GN ORFNames=BCE_G9241_1372;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Rillstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RA "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax.";
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RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454 (2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SIMILARITY: Belongs to the ABC transporter family.
CC -----
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CC -----
DR EMBL; AAEK0100009; EALJ5130.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Nucleotide-binding; Transport.
SQ SEQUENCE 300 AA; 33506 MW; E0811D19DB91DC53 CRC64;

Query Match 50.9%; Score 785; DB 2; Length 300;
Best Local Similarity 53.9%; Pred. No. 2.5e-36;
Matches 160; Conservative 55; Mismatches 74; Indels 8; Gaps 3;

QY 4 LLEKNVSTIRKGIIEGLSPDVRAGEIFGFLGPNAGKTTTIRMIVGHMSTAGEIAV 63
DB 5 VVKLENVRKIKGTEIIRGLSFVEVGEVYGLGPNAGKTTTIRMIVGHMSTAGEIAV 64
QY 64 CGVSVKENPEKAAHIGAIVENPELYKFLTYGNLQOYARMT-KGYTKKKIDIEIVLVL 122
DB 65 CGHSIRTEREKALEQIGAIVENPELYDYMTGMQNLKHPANMAITPISKERIAIIVKLVEL 124
QY 123 KNRINDKVTYSYSLGMRQRLGSLHDPKLLILDEPTNGLDPAGIREIDYLRKLTREK 182
DB 125 EHAHKKVKVTSYSLGMRQRLGSLHDPKLLILDEPTNGLDPAGIREIDYLRKLTREK 184
QY 183 GMAVIVSSHLLSEMLMCDRIALIQNGKLRIQHVHGPAR-DEKKRYYYQADDTQALTRE 241
DB 185 NIATIVSSHLLSEMLMCDRIALIQNGKLRIQHVHGPAR-DEKKRYYYQADDTQALTRE 241
QY 242 AAARFKVKVDEAGG-IEISIQKDEVDPLIKHLTDSGVRLYEYKAVNKSLDEDFLEIT 298
DB 240 --KANEIIKGAQNVIVSVTKKEIPQLVKLVNEDVLVYGVTVQNKLTLEDEFLAIT 295

RESULT 7
Q73BE3_BACCI PRELIMINARY; PRT; 300 AA.
AC Q73BE3_
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE ABC transporter, ATP-binding protein.
GN ORFNames=BCE_1475;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.B., Fraser C.W., Read T.D.;
RA "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988 (2004).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
CC -----
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DR ENBL; AE017194; AAS40404.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016987; F:ATPase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR DR InterPro; IPR003593; AAA_ATPase.
DR DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF00005; ABC_tran; 1.
DR DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR DR ATP-binding; Complete proteome; Nucleotide-binding; Transport.
DR SK SEQUENCE 300 AA; 33353 MW; 5941DAE7B78DD7A7 CRC64;

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Query Match 50.9%; Score 785; DB 2; Length 300;
Best Local Similarity 53.4%; Pred. No. 2.5e-36;
Matches 159; Conservative 60; Mismatches 69; Indels 10; Gaps 4;

[illegible]

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RESULT 8
Q3EWL1_BACTI PRELIMINARY; PRT; 300 AA.
ID Q3EWL1_BACTI
AC Q3EWL1;
DT 08-NOV-2005, integrated into UniprotKB/TREMBL.
DT 08-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Bactitracin transport ATP-binding protein bcrA.
GN ORFNames=RBTH 02680;
GN Bacillus thuringiensis serovar israelensis ATCC 35646.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=339854;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35646;
RA Anderson I., Sorokin A., Kapratral V., Reznik G., Bhattacharya A.,
RA Mikhailova N., Burd H., Joukov V., Kaznadzey D., Walunas T.,
RA D'Souza M., Larsen N., Pusch G., Liolios K., Grechkin Y., Lapidus A.,
RA Goltzman E., Chu L., Fonstein M., Ehrlich D., Overbeek R.,
RA Kyrpides N., Ivanova N.;
RT "Comparative genome analysis of Bacillus cereus group genomes with
RT Bacillus subtilis.";
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! SIMILARITY: Belongs to the ABC transporter family.
CC -----
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CC      ENBL; AAJMJ000404; EAO52546.1; Genomic_DNA.
DR      GO; GO:0005524; P:ATP binding; IEA.
DR      GO; GO:0005524; P:ATP binding; IEA.
DR      GO; GO:0016887; P:ATPase activity; IEA.
DR      GO; GO:0001666; P:nucleotide binding; IEA.
DR      GO; GO:0006810; P:transport; IEA.
DR      InterPro; IPR003593; AAA_ATPase.
DR      InterPro; IPR003439; ABC_transp_like.
DR      Pfam; PF00005; ABC_tran; 1.
DR      ProDom; PD000006; ABC_transporter; 1.
DR      SMART; SM00382; AAA_1.
DR      PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR      PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
DR      KW ATP-binding; Nucleotide-binding; Transport.
DR      SQ SEQUENCE 300 AA; 33369 MW; 841D6E496F197457 CRC64;

Query Match          50.8%; Score 784; DB 2; Length 300;
Best Local Similarity 53.4%; Pred. No. 2.9e-36;
Matches 159; Conservative 58; Mismatches 71; Indels 10; Gaps 4;

Qy      4 LLELKNVSKTIRGKIIIEGLSFDVRAGEIFGFLGPNAGAKTTTIRMIVGHMSITAGEIAV 63
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      5 VVKLENVRKRIEGTEIIRGLSPFREVGEVYVGFGLGPNSGKTTTIRMVTLGLISWTEGDI 64

Qy      64 CGVSVKENTEKAARHGAIVENDELKYFLTYGYNLQOYARMT-KGVTKKKIDIVELVGL 122
      :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      65 CGHSIRSERKALEQICAVENPELDYMTGMQLKHFANMAIKPISKERIAEIVKLVEL 124

Qy      123 KNRINDKVTYSIGMQRGLQASLHDPKLLILDEPTNGLDPAGIRETRDYLRKLRTREK 182
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      125 EHAHKKVKVTYSIGMKQRGLGIAQLLHPKLLILDEPTNGLDPAGIRQIRDYLRQAKEE 184

Qy      183 GMATIVSSHLLSEMELMCDRIAIIQNGKLRDIOHVHGPAR-DEKKRYIYQADDTQALTR 241
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      185 NIATIVSSHLLSEIELMCDRVIIKGEFVQEYNLHEKVKHGDEAVVVADEVDEVQKA--- 241

Qy      242 AAARFKVKVDEABGG-IELSIQKDEVPDILKHLTDSGVRLEYEYKAVNKSLEDRFLEIT 298
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      242 ----NBIIGKAGNIVASLTQNTIPQVKKLVHADVLVYGVTVQNKLTLEDEFLAIT 295

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RESULT 9

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063E15_BACCZ PRELIMINARY; PRT; 300 AA.
AC Q63E15;
AC Q63E15;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE ABC transporter, ATP-binding protein; possible multidrug transporter.
DE Name=BCRA; OrderedAccession=BC3361248;
GN Bacillus cereus (strain ZK / E33L).
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OC NCBI_TaxID=288681;
OX [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Kaim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: Belongs to the ABC transporter family.
-----
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-----
CC EMBL: CP000001; AAU19000.1; -; Genomic_DNA.
CC GO: GO:0005524; F:ATP binding; IEA.
CC GO: GO:0015887; F:ATPase activity; IEA.
CC GO: GO:0000166; F:nucleotide binding; IEA.
CC GO: GO:0006810; P:transport; IEA.
CC InterPro: IPR003593; AAA ATPase.
CC InterPro: IPR003439; ABC transp like.

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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Raeko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to *Bacillus anthracis* pXOI.";
RL Nucleic Acids Res. 32:977-988(2004).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
CC -----
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CC -----
CC EMBL: AE017194; AAS44429.1; -; Genomic_DNA.
DR GO: GO:0005224; F:ATP binding; IEA.
DR GO: GO:0016887; F:ATPase activity; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_tranap_like.
DR Pfam: PF00005; ABC_tran; 1.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR PROSITE: PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.
KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.
SQ SEQUENCE 305 AA; 34406 MW; FDEEA942E1DFF99A CRC64;

Query Match 48.2%; Score 743.5; DB 2; Length 305;
Best Local Similarity 47.8%; Pred. No. 5.5e-34;
Matches 150; Conservative 68; Mismatches 77; Indels 19; Gaps 3;

QY 1 LETLLELKVNYSKTRIGKRIEGLSFDFVRAGEIFGFLGPNAGAKTTTIRMVGHMSITAGE 60
DB 1 MTTILSVRDVKVIGNTKLVENISFDVTQGEVFGFLGPNAGAKTTTIRMVGLIKATEGT 60

QY 61 IAVCGSVKCNFEKAARHICAIVENPELYKFTCYQNLQYARMTKGVTKKKIDEIVELV 120
DB 61 ISIGYSIKENFRFAMRQIGSVENPELYTLTGWENLKQFARMLGDISDRIMEIAQMV 120

QY 121 GLKNRIKNDKVTYSLGMRQRLGLAQSLHDPKLLILDEPTNGLDPAGIREIDVLRKLTR 180
DB 121 HLDERIHDKVTYSLGMRQRLGLAQSLHDPKLLILDEPTNGLDPAGIREIDVLRKLTR 180

QY 181 EKGMAVIVSSHLSAMELMCDRIAIIONGKLURDIOHVHGPARDKKRY-YIQADDTQALT 239
DB 181 EENMSVFISHLSEVMQICDRVAIHKKGMITVAKVEELIKTASDRVEWIVTPIGKA-- 238

QY 240 REAAAFPKVKVDEAGGIELSIQKD-----EVPDLIKHLTDSGVRLVEVKAVNKS 290
DB 239 -----KMLEDAEAEVREVSIEGDRLLCRNVIASISNNWKFVENEIDVHSVKELVFTL 291

QY 291 EDRELEITADKEEA 304
DB 292 EDLFIELTRGEQHA 305

RESULT 15
Q4MLR2_BACCE PRELIMINARY; PRT; 305 AA.
AC Q4MLR2;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Bacitracin transport ATP-binding protein bcrA.
GN ORFNames=BCE.G9241.5584;
OS *Bacillus cereus* G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC *Bacillus cereus* group.
OX NCBI_taxid=269801;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2006, 13:49:18 ; Search time 50 Seconds
(without alignments)
537.438 Million cell updates/sec

Title: US-10-510-941-2

Perfect score: 1542

Sequence: 1 LETLLEKNVSKIRGKKII.....KSLDRLEITADKRAQHV 307

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /EMC_Celerra_SID33/ptodata/2/iaa/6 COMB.pcp.*
3: /EMC_Celerra_SID33/ptodata/2/iaa/7 COMB.pcp.*
4: /EMC_Celerra_SID33/ptodata/2/iaa/H COMB.pcp.*
5: /EMC_Celerra_SID33/ptodata/2/iaa/PTCTUS COMB.pcp.*
6: /EMC_Celerra_SID33/ptodata/2/iaa/RE COMB.pcp.*
7: /EMC_Celerra_SID33/ptodata/2/iaa/baCKfilea1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	455.5	29.5	310	2	US-09-107-532A-6910
2	436	28.3	233	2	US-09-627-376-12
3	436	28.3	233	2	US-10-047-676B-12
4	430.5	27.9	332	2	US-09-107-532A-3752
5	416.5	27.0	303	2	US-09-107-532A-5192
6	410	26.6	345	2	US-09-252-991A-31957
7	408.5	26.5	330	2	US-09-902-540-15345
8	407.5	26.4	319	2	US-09-758-759-89
9	397	25.7	328	2	US-09-902-540-10796
10	396.5	25.7	309	2	US-09-252-991A-21204
11	392.5	25.5	215	2	US-09-583-110-2846
12	392.5	25.5	229	2	US-09-107-433-3116
13	391.5	25.4	309	2	US-09-902-540-16586
14	384.5	24.9	228	2	US-09-602-787A-402
15	381	24.7	788	2	US-09-252-991A-28171
16	374.5	24.3	240	2	US-09-902-540-15786
17	373	24.2	292	2	US-09-602-787A-352
18	371.5	24.1	290	2	US-09-902-540-16248
19	371.5	24.1	594	2	US-09-543-681A-5528
20	367	23.8	588	2	US-09-489-039A-13579
21	363.5	23.6	315	2	US-09-134-000C-6449
22	362.5	23.5	245	2	US-09-902-540-13001
23	354.5	23.0	248	2	US-09-710-279-3218
24	352.5	22.9	316	2	US-09-902-540-10994
25	349.5	22.7	1272	2	US-09-949-016-7472
26	347.5	22.5	2059	3	US-10-114-270-176

27	347.5	22.5	2144	2	US-10-154-419-2	Sequence 2, Appli
28	347.5	22.5	2146	2	US-09-949-016-6947	Sequence 6947, Ap
29	346.5	22.5	1684	2	US-08-665-259-25	Sequence 25, Appl
30	346.5	22.5	1684	2	US-08-762-500-25	Sequence 25, Appl
31	346.5	22.5	1704	2	US-08-762-500-75	Sequence 75, Appl
32	346.5	22.5	1704	2	US-09-032-438C-120	Sequence 120, App
33	346.5	22.5	1766	2	US-09-949-016-10796	Sequence 10796, A
34	345.5	22.4	304	2	US-09-107-532A-5424	Sequence 5424, Ap
35	344.5	22.3	607	2	US-09-252-991A-18351	Sequence 18351, A
36	344	22.3	257	2	US-09-107-532A-4066	Sequence 4066, Ap
37	342.5	22.2	205	2	US-09-134-001C-4766	Sequence 4766, Ap
38	341.5	22.1	254	2	US-09-107-532A-4983	Sequence 4983, Ap
39	341	22.1	291	2	US-09-107-532A-4205	Sequence 4205, Ap
40	340	22.0	323	2	US-09-489-039A-12496	Sequence 12496, A
41	339.5	22.0	589	2	US-09-328-352-7592	Sequence 7592, Ap
42	339	22.0	317	2	US-09-583-110-5279	Sequence 5279, Ap
43	339	22.0	327	2	US-09-107-433-3331	Sequence 3331, Ap
44	335	21.7	315	2	US-09-328-352-4388	Sequence 4388, Ap
45	334.5	21.7	2273	2	US-09-032-438C-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-107-532A-6910
; Sequence 6910, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6910:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...310
; SEQUENCE DESCRIPTION: SEQ ID NO: 6910:

US-09-107-532A-6910

Query Match 29.5%; Score 455.5; DB 2; Length 310;
Best Local Similarity 34.8%; Pred. No. 7.2e-36;
Matches 104; Conservative 79; Mismatches 107; Indels 11; Gaps 6;

QY 2 ETLLKLVKVTIRGKKIIEGLSFDVRAGEIFGLGPNAGAGKTTTIRMIVGHMSITAGEI 61
DB 11 ETVLKATGTTKKYGAALKDKVIEIKRGMIVGLIGENGAGKSTFTMTIIGLSIDEGSI 70
QY 62 AVCGSVKVFENFEKAARHIGAIVENPELYKFLTYQNLQOYARMTKGVTKKKIDEIVELVG 121
DB 71 ELFGTT--DLQAARRMGQSIETPALYPELTARDNLRIQA-ANGGVSDREIBDLKQMR 126
QY 122 LKNRINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 181
DB 127 LENTGKKKAKNFSGLMRQRLAIANALITNPEFLILDEPTNGLDPAGMAENREIIRQLVKE 186
QY 182 KGMVIVSSHLLSEMELMCDRIAIQNGKLRDIOHVHGPARDKKRYIQADDT---QAL 238
DB 187 RGITVLLSSHLDELQIATHYGLHEGL--IKELSKBELAQESRQFIKIDTSATEQAV 244
QY 239 T-REAAAFKVKVDEAGGIELSIQKDEVPDLIKHLTDSGVRLYEYKAVNKSLEDRLEI 297
DB 245 TVLDSLGRYDYFV-QSSRVQLFEGIDQVAAINQALVEAKVPVDGIHLVQGKLEDFLOL 303
QY 298 T 298
DB 304 T 304

RESULT 2

US-09-627-376-12
; Sequence 12, Application US/09627376

; Patent No. 6342385

; GENERAL INFORMATION:

; APPLICANT: Qi, Fengxia Caufield, Page Chen, Ping

; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS

; FILE REFERENCE: UAB-17402/22

; CURRENT APPLICATION NUMBER: US/09/627,376

; CURRENT FILING DATE: 2001-05-30

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 12

; LENGTH: 233

; TYPE: PRT

; ORGANISM: Streptococcus mutans

US-09-627-376-12

Query Match 28.3%; Score 436; DB 2; Length 233;
Best Local Similarity 41.5%; Pred. No. 3.7e-34;
Matches 93; Conservative 51; Mismatches 72; Indels 8; Gaps 4;

QY 1 LETLLEKLVKVTIRGKKIIEGLSFDVRAGEIFGLGPNAGAGKTTTIRMIVGHMSITAGEI 60
DB 1 MDYMLETKNLTKQFGKQTAVNQLNKLKVERHSIYGLLGPNGSGKSTTLKMITGMLRKTSGH 60
QY 61 IAVCGSVKVFENFEKAARHIGAIVENPELYKFLTYQNLQOYARMTKGVTKKKIDEIVELV 120
DB 61 ILIDG---HDWSRKDLNIGALIESPPLYENLTARENKLVRTLML-GLPDSRIDEVLKIV 116
QY 121 GLKNRINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 180
DB 117 DLNTGKKRAGQFSMGKQRLGIAIALNSPQLLILDEPTNGLDPGIGQLRNLRSFPT 176
QY 181 EKMVIVSSHLLSEMELMCDRIAIQNGKLRDIOHVHGPARD 224
DB 177 Q-GITVIISHSILSEIQMTADHIGIANGVLGYQDRIH---QDE 216

RESULT 3

US-10-047-676B-12

; Sequence 12, Application US/10047676B

; Patent No. 6699970

; GENERAL INFORMATION:

; APPLICANT: Qi, Fengxia

; APPLICANT: Caufield, Page W.

; APPLICANT: Chen, Ping

; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS

; FILE REFERENCE: UAB-17403/22

; CURRENT APPLICATION NUMBER: US/10/047,676B

; CURRENT FILING DATE: 2002-01-14

; PRIOR APPLICATION NUMBER: US 09/627,376

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 12

; LENGTH: 233

; TYPE: PRT

; ORGANISM: Streptococcus mutans

US-10-047-676B-12

Query Match 28.3%; Score 436; DB 2; Length 233;
Best Local Similarity 41.5%; Pred. No. 3.7e-34;
Matches 93; Conservative 51; Mismatches 72; Indels 8; Gaps 4;

QY 1 LETLLEKLVKVTIRGKKIIEGLSFDVRAGEIFGLGPNAGAGKTTTIRMIVGHMSITAGEI 60
DB 1 MDYMLETKNLTKQFGKQTAVNQLNKLKVERHSIYGLLGPNGSGKSTTLKMITGMLRKTSGH 60
QY 61 IAVCGSVKVFENFEKAARHIGAIVENPELYKFLTYQNLQOYARMTKGVTKKKIDEIVELV 120
DB 61 ILIDG---HDWSRKDLNIGALIESPPLYENLTARENKLVRTLML-GLPDSRIDEVLKIV 116
QY 121 GLKNRINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 180
DB 117 DLNTGKKRAGQFSMGKQRLGIAIALNSPQLLILDEPTNGLDPGIGQLRNLRSFPT 176
QY 181 EKMVIVSSHLLSEMELMCDRIAIQNGKLRDIOHVHGPARD 224
DB 177 Q-GITVIISHSILSEIQMTADHIGIANGVLGYQDRIH---QDE 216

RESULT 4

US-09-107-532A-3752

; Sequence 3752, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 7310

; CORRESPONDENCE ADDRESS:

; ADDRESSER: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD/ROM ISO9660

; OPERATING SYSTEM: <Unknown>

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107,532A

; FILING DATE: 30-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/085,598

; FILING DATE: 14 May 1998

; APPLICATION NUMBER: 60/051571

; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Ariniello, Pamela Deneke

; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-012

TYPE: PRT

```
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31957

Query Match          26.6%; Score 410; DB 2; Length 345;
Best Local Similarity 29.5%; Pred. No. 2.2e-31;
Matches 94; Conservative 77; Mismatches 116; Indels 32; Gaps 6;

QY 2 ETLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGEI 61
Db 36 ETWIDIDRLSKRFSRTVNDLSFRIDRGEIVGLLGNAGKSTTLKMLSGFLAPSAGSV 95

QY 62 AVCVSKENFEKAARHIGAIVENPELY-----KFLTGYNLQOQVARTKGVTKKIDE 115
Db 96 RIFQFMDQKARQAQLGLYLPENAFSYGEMTVGEFLAFVASIRDYSGREK---RRIDS 152

QY 116 IVELVGLKNRINKVKTYSLGMRQRLGLAQLSLHDPKLLILDEPTNGLDPPAGIREIDYL 175
Db 153 AMDCMELRDERRRIETLSGFKRRVALAQAILHDPFELLLEDEPTDGLDPNQKHQVRLV 212

QY 176 RKLTRKGMNAVIVSSHLLSEMELMCDRIAIQNGKLRDIOHVHGPARDEKKRYIQADDT 235
Db 213 KNLSESK--IVVISTHILEEVSFMCSEALVINGRLL-ADNTPGELRTRSRVHHAVLSGI 269

QY 236 QALTREAAAFKVKVDEAEG-----GIELSIQKDEVPDLIKHLTDSGVRLY 281
Db 270 EAPVDPFLAIVLPGVAGIEGRPDRAAGTTLTILAPGVQI-----LPALNRLIHGSGWRVS 323

QY 282 EVKAVNKSLEDRFLEITAD 300
Db 324 GVRTEHGQLEEVPRQLTRE 342

RESULT 7
US-09-902-540-15345
; Query Match          26.4%; Score 407.5; DB 2; Length 319;
; Best Local Similarity 32.0%; Pred. No. 3.4e-31;
; Matches 101; Conservative 65; Mismatches 125; Indels 25; Gaps 8;
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15345
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15345

Query Match          26.5%; Score 408.5; DB 2; Length 330;
Best Local Similarity 31.5%; Pred. No. 2.9e-31;
Matches 100; Conservative 71; Mismatches 109; Indels 37; Gaps 7;

QY 2 ETLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGEI 61
Db 12 QPLLQLEGLTRFRFKGRTAVDGLSVRPGIEILGLLGNAGKSTTFQVLAGLLSPAGLV 71

QY 62 AVCVSKENFEKAARHIGAIVENPELYKFLTGYNLQOQVARTKGV---TKKKIDEIV 117
Db 72 RFEGRELSDDPSLRQNGIIFQSSLDLLTARENILMGLARL-YLGGGERAREREVAML 130

QY 118 ELVGLKNRINKVKTYSLGMRQRLGLAQLSLHDPKLLILDEPTNGLDPPAGIREIDYLRK 177
Db 131 SLIGLADRGDERVSTWGGMRRLLELALRVHQPVLLMDPTQGLDEAAFRFTWAHLKR 190

QY 178 LTRKGMNAVIVSSHLLSEMELMCDRIAIQNGK-----RDIOHVHGPARD 223
Db 191 LRDSSEGLTVLLTTHRADEAD-VCDRVLAVDAGKLVACDTPQALASRWGGDILSV----- 243

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31957

Query Match          26.6%; Score 410; DB 2; Length 345;
Best Local Similarity 29.5%; Pred. No. 2.2e-31;
Matches 94; Conservative 77; Mismatches 116; Indels 32; Gaps 6;

QY 2 ETLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGEI 61
Db 36 ETWIDIDRLSKRFSRTVNDLSFRIDRGEIVGLLGNAGKSTTLKMLSGFLAPSAGSV 95

QY 62 AVCVSKENFEKAARHIGAIVENPELY-----KFLTGYNLQOQVARTKGVTKKIDE 115
Db 96 RIFQFMDQKARQAQLGLYLPENAFSYGEMTVGEFLAFVASIRDYSGREK---RRIDS 152

QY 116 IVELVGLKNRINKVKTYSLGMRQRLGLAQLSLHDPKLLILDEPTNGLDPPAGIREIDYL 175
Db 153 AMDCMELRDERRRIETLSGFKRRVALAQAILHDPFELLLEDEPTDGLDPNQKHQVRLV 212

QY 176 RKLTRKGMNAVIVSSHLLSEMELMCDRIAIQNGKLRDIOHVHGPARDEKKRYIQADDT 235
Db 213 KNLSESK--IVVISTHILEEVSFMCSEALVINGRLL-ADNTPGELRTRSRVHHAVLSGI 269

QY 236 QALTREAAAFKVKVDEAEG-----GIELSIQKDEVPDLIKHLTDSGVRLY 281
Db 270 EAPVDPFLAIVLPGVAGIEGRPDRAAGTTLTILAPGVQI-----LPALNRLIHGSGWRVS 323

QY 282 EVKAVNKSLEDRFLEITAD 300
Db 324 GVRTEHGQLEEVPRQLTRE 342

RESULT 8
US-09-758-759-89
; Query Match          26.4%; Score 407.5; DB 2; Length 319;
; Best Local Similarity 32.0%; Pred. No. 3.4e-31;
; Matches 101; Conservative 65; Mismatches 125; Indels 25; Gaps 8;
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: ID0983K US
; CURRENT APPLICATION NUMBER: US/09/758,759
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/175,751
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 89
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Micromonospora carbonacea
; FEATURE:
; OTHER INFORMATION: evbc
US-09-758-759-89

Query Match          26.4%; Score 407.5; DB 2; Length 319;
Best Local Similarity 32.0%; Pred. No. 3.4e-31;
Matches 101; Conservative 65; Mismatches 125; Indels 25; Gaps 8;

QY 4 LLELKNVSKTIRGK-----KIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMS 55
Db 1 MIQTGLRKSFRSRAGRQHKTVDAVRGVDLDAEAGEIFGFLGPNAGKTTTLMLATLIT 60

QY 56 ITAGEIACVGVSKENFEKAARHIGAIVENPELYKFLTGYNLQOQVARTKGVTK---K 111
Db 61 PDGGQATIAAGADLLRNPAEVRRIQVYAAQSGTWDSTAREELVTLHARM-YGIGKADALR 119

QY 112 KIDEIVELVGLKNRINKVKTYSLGMRQRLGLAQLSLHDPKLLILDEPTNGLDPPAGIREI 171
Db 120 RAERALLAARFQTEYADRKCKTYSGGQRRRVEALGIIHDPRIVFLDEPTSGLDPPQSAHM 179

QY 172 RDLRKLTRKGMNAVIVSSHLLSEMELMCDRIAIQNGKLRDIOHVHGPARDEKKRYIQ 231
Db 180 WDEIRRL-RAEGMTVFITTHYLDEADALCDRIAMDHGEVVAEGTGGPKLREISGEVLLV 238

QY 232 ADTQALTREAAAFK-----VKVDEAEGEIELSIQKDE-----VPDLIKHLTDSGVRLYE 282
Db 239 GLDA-AATPAAQLLDTPEYVTKLETVDGG-GLRLTVDEGATAIPQVLRRLDQSGURLSS 296

QY 283 KVAVNKSLEDRFLEIT 298
Db 297 IELHRPSLDVFLTKT 312

RESULT 9
US-09-902-540-10796
; Query Match          26.4%; Score 407.5; DB 2; Length 319;
; Best Local Similarity 32.0%; Pred. No. 3.4e-31;
; Matches 101; Conservative 65; Mismatches 125; Indels 25; Gaps 8;
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: ID0983K US
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/175,751
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 89
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Micromonospora carbonacea
; FEATURE:
; OTHER INFORMATION: evbc
US-09-758-759-89

Query Match          26.4%; Score 407.5; DB 2; Length 319;
Best Local Similarity 32.0%; Pred. No. 3.4e-31;
Matches 101; Conservative 65; Mismatches 125; Indels 25; Gaps 8;

QY 4 LLELKNVSKTIRGK-----KIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMS 55
Db 1 MIQTGLRKSFRSRAGRQHKTVDAVRGVDLDAEAGEIFGFLGPNAGKTTTLMLATLIT 60

QY 56 ITAGEIACVGVSKENFEKAARHIGAIVENPELYKFLTGYNLQOQVARTKGVTK---K 111
Db 61 PDGGQATIAAGADLLRNPAEVRRIQVYAAQSGTWDSTAREELVTLHARM-YGIGKADALR 119

QY 112 KIDEIVELVGLKNRINKVKTYSLGMRQRLGLAQLSLHDPKLLILDEPTNGLDPPAGIREI 171
Db 120 RAERALLAARFQTEYADRKCKTYSGGQRRRVEALGIIHDPRIVFLDEPTSGLDPPQSAHM 179

QY 172 RDLRKLTRKGMNAVIVSSHLLSEMELMCDRIAIQNGKLRDIOHVHGPARDEKKRYIQ 231
Db 180 WDEIRRL-RAEGMTVFITTHYLDEADALCDRIAMDHGEVVAEGTGGPKLREISGEVLLV 238

QY 232 ADTQALTREAAAFK-----VKVDEAEGEIELSIQKDE-----VPDLIKHLTDSGVRLYE 282
Db 239 GLDA-AATPAAQLLDTPEYVTKLETVDGG-GLRLTVDEGATAIPQVLRRLDQSGURLSS 296

QY 283 KVAVNKSLEDRFLEIT 298
Db 297 IELHRPSLDVFLTKT 312
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; FILE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; TITLE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16586
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; US-09-902-540-16586

Query Match          25.4%   Score 391.5; DB 2; Length 309;
Best Local Similarity 32.8%; Pred. No. 1.2e-29;
Matches 105; Conservative      62; Mismatches 118; Indels    35; Gaps

Qy  4 LLELKNVSKTIRGKKIIIGLSFQVRAGEIFGFGLPGNGAGKTTTIRMIVGHMSITAGEIAV 63
Db       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  1 MIQVEGLTKYVGHAARELAFTISQGEVIGFLGNGAGKSTTLKVLGCVLMPSTGRVVI 60
Db       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  64 CGVSVKENFEKAARHGAIVENPELYKFLTCYONLQQVARMTKGVTK---KIDEIVEL 119
Db       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  61 DGHVVNSAHEVRORIQLDPVPPLDEMTVGEYL-TYAQLRGVTSRDTASRVGEAEK 119
Db       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  120 VGLKNRINDKVITYSLGMQRGLQAQLLHDHPKLILDEPTNGLDPPAGIREIRDYLRKLT 179
Db       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  120 TGLRDVHGELISTLSHGVRQGVQAALVHKPALLILDPTSGLDPRQIVEMRDVIRGL- 178
Db       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  180 REKGW-AVIVSSHLSELMCDRIALIQNG-----KLRDIQHVGHPARDEK 225
Db       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  179 --KGATLVSSHTLPISOTCDRLLIHHKMLVAQGTEELAAKGGRTIELEVRGBK 236
Db       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  226 KRYVIQADDTOALTREAAAFKRVKDVAEGG-IELSIO--KDEVLDLIKHLTDSGVRLYE 282
Db       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  237 AR-----AVEVLQR----FGSVEVDRASDGLVALTVRAFPQRPQAVAVVGAGLELLR 286
Db       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  283 VKAVNKSLSDRFLEITADKE 302
Db       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy  287 LDQAGAQLESIFLRLTHQE 306
Db       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-09-602-787A-402
Sequence 402, Application US/09602787A
Patent No. 6696561
GENERAL INFORMATION:
APPLICANT: Pompejus, Mark
APPLICANT: Krüger, Burkhard
APPLICANT: Schöder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauser, Gregor
TITLE OF INVENTION: CORNYEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: TRANSPORT
FILE REFERENCE: BGI-125CP
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: USSN 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931454.3
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931478.0
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931563.9
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932122.1
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932124.8
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
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; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932180.9
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932182.5
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932190.6
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932191.4
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932209.0
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932212.0
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932227.9
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932228.7
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932229.5
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932230.9
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932927.3
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19933005.0
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19933006.9
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19940764.9
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: DE 19940765.7
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: DE 19940766.5
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: DE 19940830.0
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: DE 19940831.9
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: DE 19940832.7
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: DE 19940833.5
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: DE 19941378.9
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: DE 19941379.7
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: DE 19941395.9
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: DE 19942077.7
 ; PRIOR FILING DATE: 1999-09-03
 ; PRIOR APPLICATION NUMBER: DE 19942078.5
 ; PRIOR FILING DATE: 1999-09-03
 ; PRIOR APPLICATION NUMBER: DE 19942079.3
 ; PRIOR FILING DATE: 1999-09-03
 ; PRIOR APPLICATION NUMBER: DE 19942088.2
 ; PRIOR FILING DATE: 1999-09-03
 ; NUMBER OF SEQ ID NOS: 678
 ; SEQ ID NO 402
 ; LENGTH: 228
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-09-602-787A-402

Query Match 24.9%; Score 384.5; DB 2; Length 228;
 Best Local Similarity 41.2%; Pred. No. 3.6e-29;
 Matches 87; Conservative 45; Mismatches 70; Indels 9; Gaps 4;
 QY 4 LLEKNVSKTIRGKIIIEGLSFQVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGEIAV 63
 Db 1 MINVEGLTKQYGVQVRAVDLSFVKPGIVTGVFLGPNAGKSTTWRLLGLDNFTAGHATI 60
 QY 64 CGV---SVKENFEKAARHGAIVENPELYKFLTYQNLOQYARMTKGVTKKKIDEIVELV 120
 Db 61 EGOPYRSLKNPLTK----VQALLDAKATHNRTAENHLKWIAR-ANGLSTKRVDEVLTIV 115

QY 121 GLKNRINDKVTYSLSGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAQIREIRDYLRKLTR 180
 Db 116 GLTGVGSKTKGFGSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAQIREIRDYLRKLTR 175
 QY 181 EKMNAVIVSSHLLSEMELMCDRIAIQNGKL 211
 Db 176 Q-GRTVLVSSHLLSEMAQTAHLIVIGRGKL 205

RESULT 15
 US-09-252-991A-28171
 ; Sequence 28171, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 28171
 ; LENGTH: 788
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-28171

Query Match 24.7%; Score 381; DB 2; Length 788;
 Best Local Similarity 31.8%; Pred. No. 4.9e-28;
 Matches 97; Conservative 57; Mismatches 111; Indels 40; Gaps 6;
 QY 3 TLELKNVSKTIRGKIIIEGLSFQVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGEIA 62
 Db 486 SLVEIDGATLYRYGALTALSGLDLRLPEGEVLGLGHNGAKTTTILVLGLLAPSEGEVR 545
 QY 63 VCGSVKNEFEKAARHGAIVENPELYKFLTYQNLOQYARMTKGVTKKKIDEIVELVGL 122
 Db 546 VLGHDAARS--LEARRQLGYPENVTYPQLSGAETLRHFAEL-KGVAPAEAAARLLEQVGL 602
 QY 123 KNRINDKVTYSLSGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAQIREIRDYLRKLTR 182
 Db 603 GHAAARRLLKTYSGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAQIREIRDYLRKLTR 661
 QY 183 GMNAVIVSSHLLSEMELMCDRIAIQNGKLRIQHVHGPARDKRYVYIQADDTQALTR 242
 Db 662 GTGIVLCSHVLPGVETHIDRAALAGRLQ-----VAGSLAELRKA 703
 QY 243 AAFPRKVKVDEAEGGIELSQKORVPDLIKHLTDSGVRVLYEVKAVNKSLEDRFLBITADKE 302
 Db 704 ALPTRVRLASPHN-----PQWLE-----RWHRAAGLAARLLDQRIEVLDDA 745
 QY 303 EAGHV 307
 Db 746 ERDGV 750

Search completed: July 13, 2006, 13:50:40
 Job time : 52 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 13, 2006, 13:49:57 ; Search time 186 Seconds
(without alignments)
764.554 Million cell updates/sec

Title: US-10-510-941-2
Perfect score: 1542
Sequence: 1 LETLLEKNVSKTIRGKKII.....KSLDRFLEITADKEAQQHV 307

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.psp.*
- 2: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.psp.*
- 3: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.psp.*
- 4: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.psp.*
- 5: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.psp.*
- 6: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.psp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1542	100.0	307	5	US-10-510-941-2
2	738.5	47.9	310	4	US-10-369-493-16618
3	734	47.6	301	4	US-10-282-122A-60404
4	734	47.6	301	6	US-11-045-004-182
5	639	41.4	306	6	US-11-045-004-885
6	638	41.4	309	5	US-10-510-386-84
7	536	34.8	302	4	US-10-282-122A-72352
8	535.5	34.7	306	4	US-10-369-493-17122
9	516	33.5	299	4	US-10-369-493-9838
10	493	32.0	306	4	US-10-369-493-20363
11	493	32.0	308	4	US-10-369-493-1297
12	491.5	31.9	318	4	US-10-369-493-1336
13	485	31.5	221	4	US-10-369-493-16570
14	473	30.7	305	4	US-10-369-493-21602
15	468	30.4	346	4	US-10-566-761-12401
16	455.5	29.5	306	4	US-10-282-122A-53430
17	447.5	29.0	377	5	US-10-282-122A-54022
18	447.5	29.0	385	4	US-10-501-282-5390
19	444	28.8	336	5	US-10-732-923-1559
20	438	28.4	311	4	US-10-369-493-11246
21	436	28.3	233	4	US-10-047-676A-12
22	436	28.3	233	5	US-10-790-914-12
23	435.5	28.2	237	4	US-10-369-493-18206
24	433.5	28.1	341	4	US-10-566-761-8470
25	432.5	28.0	310	4	US-10-282-122A-52344
26	431.5	28.0	305	4	US-10-369-493-18115
27	431.5	28.0	316	4	US-10-369-493-18754

28	431.5	28.0	339	5	US-10-732-923-1502	Sequence 1502, Ap
29	431.5	28.0	443	4	US-10-156-761-10399	Sequence 10399, A
30	431	28.0	308	4	US-10-156-761-14601	Sequence 14601, A
31	430.5	27.9	233	4	US-10-369-493-11165	Sequence 11165, A
32	429	27.8	312	3	US-09-738-626-6521	Sequence 6521, Ap
33	426.5	27.7	300	6	US-11-079-463-8196	Sequence 8196, Ap
34	425	27.6	308	4	US-10-369-493-16655	Sequence 16655, A
35	424.5	27.5	312	4	US-10-369-493-1202	Sequence 1202, Ap
36	424.5	27.5	316	4	US-10-369-493-20198	Sequence 20198, A
37	424.5	27.5	339	5	US-10-732-923-1771	Sequence 1771, Ap
38	422.5	27.4	310	5	US-10-732-923-1537	Sequence 1537, Ap
39	421.5	27.3	221	4	US-10-369-493-11149	Sequence 11149, A
40	421.5	27.3	310	4	US-10-369-493-17283	Sequence 17283, A
41	421	27.3	327	4	US-10-369-493-3029	Sequence 3029, Ap
42	420.5	27.3	248	5	US-10-474-792-392	Sequence 392, App
43	420.5	27.3	282	4	US-10-369-493-17469	Sequence 17469, A
44	420	27.2	312	4	US-10-369-493-1262	Sequence 1262, Ap
45	419	27.2	229	4	US-10-369-493-9672	Sequence 9672, Ap

ALIGNMENTS

RESULT 1
US-10-510-941-2
; Sequence 2, Application US/10510941
; Publication NO. US20060040346A1
; GENERAL INFORMATION:
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Olesen, Peter Bjarke
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10297.204-US
; CURRENT FILING DATE: 2004-10-08
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-941-2

Query Match	100.0%;	Score 1542;	DB 5;	Length 307;
Best Local Similarity	100.0%;	Pred. No. 6.9e-123;		
Matches 307;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	LETLLEKNVSKTIRGKKII	EGLSFDVRAGEIFGFLGPNAGKTTTIRMI	VGHMSITAGE 60
Db	1	LETLLEKNVSKTIRGKKII	EGLSFDVRAGEIFGFLGPNAGKTTTIRMI	VGHMSITAGE 60
Qy	61	IAVCGSVKENFEKAARHIGAI	VENPELYKFLGYQNLQOYARMTKGVTKKKID	EIVELV 120
Db	61	IAVCGSVKENFEKAARHIGAI	VENPELYKFLGYQNLQOYARMTKGVTKKKID	EIVELV 120
Qy	121	GLKNRNDKVTYSLGMRQRLGLA	QSLHDPKLLIDEPNGLDPPAGIREIRDLRLK	TR 180
Db	121	GLKNRNDKVTYSLGMRQRLGLA	QSLHDPKLLIDEPNGLDPPAGIREIRDLRLK	TR 180
Qy	181	EKGMAVIVSHLLSELMCDRI	TAIQNGKLRDIOHVHGPAREKRYIQAADTQAL	TR 240
Db	181	EKGMAVIVSHLLSELMCDRI	TAIQNGKLRDIOHVHGPAREKRYIQAADTQAL	TR 240
Qy	241	EAAPFRKVKVDEAGGIELSI	QKDEVPDLIKHLTDSGRLVYEKAVNKSL	EDRPLEITAD 300
Db	241	EAAPFRKVKVDEAGGIELSI	QKDEVPDLIKHLTDSGRLVYEKAVNKSL	EDRPLEITAD 300
Qy	301	KEBAQHV 307		
Db	301	KEBAQHV 307		

; Sequence 1297, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1297
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Pyrococcus horikoshii
US-10-369-493-1297

Query Match 32.0%; Score 493; DB 4; Length 308;
Best Local Similarity 36.4%; Pred. No. 1.7e-33;
Matches 118; Conservative 67; Mismatches 91; Indels 48; Gaps 7;

QY 5 LELKNVSKTIRGKIIIEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSITAGIACV 64
DB 4 IEVEKUTSKYGFKAIDNLSFVVDGIVGFLGPNAGAGKTTTILSMGLIIPDSGQVRIL 63

QY 65 GSVSVKFNFEKAARHIGAIIVENPELYKFLTYGQNLQOYA---RMTKGVTKKKIDIEIVELVG 121
DB 64 GYDIFKEPLKAKERLGLPENAIYBELTAWRNLDFFAFSPYRMSKQEKRIEELKLVG 123

QY 122 LKNRINDKVTYSLGMRQRLGLAQSLHDPKLLILDEPTNGLDPAGIREIRYLRKLTRE 181
DB 124 LWDVRYRKAKTFSGMRQRLLAQALINDPELLILDEPTSGLDPEGARLVKDIIRE-QRK 182

QY 182 KGMVAVSSHLLSEMELMCDRIAIIONGKLRDIQHVHGPARDKRYIQAADTQALTR 241
DB 183 OGKTVFSSHLSVELADKVGIIYVKGKLRV---GTLEEIKQY-----ME 227

QY 242 AAFKRVKVDKDEAGGIELSTQKDEVPDLK-----HLTDSGV 278
DB 228 LEGY-BIKETKQPLPEL-----EIPDIIRIETKTENKAIIFAKSDIRESISELAKGI 281

QY 279 RLYEVKAVNKSLEDRFLEITADKE 302
DB 282 TIISLEIEPSLEDFLTKTYRRE 305

RESULT 12
US-10-369-493-1336
; Sequence 1336, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1336
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Pyrococcus horikoshii

US-10-369-493-1336

Query Match 31.9%; Score 491.5; DB 4; Length 318;
Best Local Similarity 35.2%; Pred. No. 2.4e-33;
Matches 112; Conservative 78; Mismatches 97; Indels 31; Gaps 7;

QY 4 LLELKNVSKTIRGKII-----IEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIV 51
DB 3 VIEVNLRK-LYPKKIPLPFRKVVEFALKGITFRVKGELFGLGPNAGAGKTTTILKILT 61

QY 52 GHMSITAGEIAVCGSVKFNFEKAARHIGAIIVENPE-LYKFLTYGQNLQOYAR---MTKG 107
DB 62 TLLEPSSGSEAKVLGVDVVKDAREIKRINLVAGERTLYRWLTAYENLRYFASIIYIPRR 121

QY 108 VTKKKIDIEIVELVGLKNRINDKVTYSLGMRQRLGLAQSLHDPKLLILDEPTNGLDPAG 167
DB 122 EAEKRIEELLNKVLWDRENDLVNYSRCMKQRLATAKALINDPEVLFLDEPTGLDQVS 181

QY 168 IREIRDYLRKLTREKGMVAVSSHLLSEMELMCDRIAIIONGKLRDIQHVHGPARDK 227
DB 182 AVFVRELVRRLVDEEGKTVLLTTHYMNEAEELCDRIAIIDHGKIIAALNTPGELKR----- 236

QY 228 YVIQADDTQALTR-----EAAAFKRVKVDKDEAGGIEL--SIOKDEVPDLKHLTDSG 280
DB 237 --WVRNDTIVEVRVRYNPGVNFGLVKVDNRGVILRGLSLEEEIPKLVFLVKSNAKV 294

QY 281 YEVKAVNKSLEDRFLEIT 298
DB 295 LSVVEKPTLEDVFIKLT 312

RESULT 13
US-10-369-493-16570
; Sequence 16570, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16570
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-369-493-16570

Query Match 31.5%; Score 485; DB 4; Length 221;
Best Local Similarity 46.2%; Pred. No. 5.2e-33;
Matches 98; Conservative 51; Mismatches 61; Indels 2; Gaps 2;

QY 1 LETLLELKNVSKTIRGKIIIEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSITAGE 60
DB 1 INTIITKTLTKVYGKQSDNININVOQGEIYGFGRNGAGKTTTIRMLLSLIKPISGT 60

QY 61 IAVCGSVKFNFEKAARHIGAIIVENPELYKFLTYGQNLQOYARMTKGVTKK-IDEIVEL 119
DB 61 IEIFGENLQKQKDIILSRIGSIIVEVGFYENLTAKENLLINAKII-GVHKNAIEEALEI 119

QY 120 VGLKNRINDKVTYSLGMRQRLGLAQSLHDPKLLILDEPTNGLDPAGIREIRYLRKLT 179
DB 120 VGLQETHETKVLGVKYSGLMKQRLGIARALLHYPELLILDEPTNGLDPTGIKEMRKLHLSLA 179

QY 180 REKGMVAVSSHLLSEMELMCDRIAIIONGKL 211

Db 180 QERNITLISSHILAEIEQLVDRIIGIIEGKL 211

RESULT 14

US-10-369-493-21602
; Sequence 21602, Application US/10369493
; Publication No. US20030233675A1

GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 21602

; LENGTH: 305

; TYPE: PRT

; ORGANISM: Pyrococcus abyssi

US-10-369-493-21602

Query Match 30.7%; Score 473; DB 4; Length 305;

Best Local Similarity 35.3%; Pred. No. 8.5e-32;

Matches 107; Conservative 77; Mismatches 103; Indels 16; Gaps 4;

Qy 4 LLELKNVSKTIRGKKIIEGLSFDVRAEIGFGLGPNAGKTTTIRMIVGHMSITAGEIAV 63
Db 3 VIEIENUTKYGKFKAVDNLSLEVEKGIIFGLGPNAGKTTTILSMGLIIPDGSVRL 62

Qy 64 CGSVKENFEKAARHIGAIVENPELYKFLTYQNLOQYA---RMTKGVTKKKIDEIVELY 120
Db 63 LGYDIFKEPIKAKERLGFLENATIEYELTAWRNLDFFASFYNIPKQEKKEKRIEELKLV 122

Qy 121 GLKNRINDKVTYSLGNRQLGIAQSLHDPKLLILDPTNGLDPPAGIREIRYLRKLT 180
Db 123 GLWDVRYRKVKSFGKMKORLLAQAALINDPELLILDPTSGLDPPQGARLVKQIILE-QK 181

Qy 181 EKMMAVTVSSHLLSEMELMCDRIAIQNGKLRDIOHVHGPARDEKKRYVIQADDTQALTR 240
Db 182 KQKTVFFSHLSVEBELADKGLIIVKGLRTVGTU-----EIKKQYMELEGEYKVE 236

Qy 241 EAAAFKRVKYE-----AEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDR 293
Db 237 TKQFPFIEPLDVIRIEKIADNKVLIIPAKSDIREILSEELSKRGITVLSLEIEPSLEDV 296

Qy 294 FLE 296

Db 297 FLK 299

RESULT 15

US-10-156-761-12401

; Sequence 12401, Application US/10156761

; Publication No. US20030119018A1

GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI

; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI

; APPLICANT: HATTORI, MASAHITO

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT APPLICATION NUMBER: US/10/156,761

; CURRENT FILING DATE: 2002-05-29

; PRIOR APPLICATION NUMBER: JP 2001-204089

; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 15109

; SEQ ID NO 12401

; LENGTH: 346

; TYPE: PRT

; ORGANISM: Streptomyces avermitilis

US-10-156-761-12401

Query Match 30.4%; Score 468; DB 4; Length 346;

Best Local Similarity 37.0%; Pred. No. 2.7e-31;

Matches 113; Conservative 54; Mismatches 114; Indels 24; Gaps 6;

Qy 10 VSKTIRGKKI-IEGLSFDVRAEIGFGLGPNAGKTTTIRMIVGHMSITAGEIAVCGYSV 68
Db 46 LTKRYRGQLAVDGLDITVPAGSVFGFLGPNAGKTTTIRMIVGHMSITAGEIAV 105

Qy 69 KENFEKAARHIGAIVENPELYKFLTYQNLOQY---ARMTKGVTKKKIDEIVELVGLKN 124
Db 106 PRSARTVLPHGALIEGPAFYGLSGRDNLLRYDAADPTADPRTTRTVAATLDRVGLTA 165

Qy 125 RINDKVTYSLGNRQLGIAQSLHDPKLLILDPTNGLDPPAGIREIRYLRKLTREKGM 184
Db 166 AAGKKAKAYSILGNKQRLGLAALIQPRLLVLDPTNGLDPPQGMREIRSLVRELASD-GT 224

Qy 185 AVIVSSHLLSEMELMCDRIAIQNGKLRDIOHVHGPARDEKKRYVIQADDTQALTREAAA 244
Db 225 TVFLSSHLLDEIEIQVCTHAAVMAQGRLLITQGAVALAAGARGRLVVTTPD----VTDA- 279

Qy 245 FRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFL 295
Db 280 ----RVLKEQGVADIIVAEEDRVVTGEPDPPDGLAELNAALVTAARVVRGFGVERASLEDAFV 335

Qy 296 EITAD 300

Db 336 ALTGE 340

Search completed: July 13, 2006, 13:53:52

Job time : 187 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 13, 2006, 13:50:52 ; Search time 29 Seconds
(without alignments)
605.617 Million cell updates/sec

Title: US-10-510-941-2
Perfect score: 1542
Sequence: 1 LETLLEKNVSKTIRGKKII.....KSLDRFLFETADKERAQHV 307

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 204771 seqs, 57208143 residues

Total number of hits satisfying chosen parameters: 204771

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New*

- 1: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 6: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	411.5	26.7	231	6	US-10-471-571A-3584
2	404.5	26.2	230	6	US-10-471-571A-1354
3	392.5	25.5	232	6	US-10-471-571A-716
4	349.5	22.7	558	7	US-11-293-697-4274
5	346.5	22.5	1704	7	US-11-289-102-341
6	338	21.9	299	6	US-10-471-571A-4370
7	331.5	21.5	949	6	US-10-449-902-43324
8	331.5	21.5	949	6	US-10-449-902-44592
9	316.5	20.5	304	7	US-11-274-683-30
10	315.5	20.5	968	6	US-10-449-902-54801
11	314	20.4	815	7	US-11-293-697-4238
12	303.5	19.7	559	7	US-11-293-697-2603
13	301.5	19.6	325	6	US-10-471-571A-3086
14	296.5	19.2	341	6	US-10-471-571A-2868
15	294	19.1	236	6	US-10-471-571A-678
16	292.5	19.0	342	6	US-10-471-571A-1718
17	292	18.9	313	6	US-10-471-571A-4896
18	287.5	18.6	199	7	US-11-133-075-62
19	275.5	17.9	423	6	US-10-471-571A-5286
20	274	17.8	365	6	US-10-471-571A-2570
21	272	17.6	302	6	US-10-471-571A-1646
22	267.5	17.3	353	6	US-10-449-902-49749
23	262.5	17.0	261	6	US-10-471-571A-496
24	254.5	16.5	282	6	US-10-471-571A-1908
25	253	16.4	364	6	US-10-471-571A-5014

26	249.5	16.2	243	6	US-10-471-571A-5186
27	249.5	16.2	692	7	US-11-056-355B-45974
28	249	16.1	298	6	US-10-471-571A-1350
29	248.5	16.1	678	7	US-11-056-355B-79452
30	245	15.9	291	6	US-10-449-902-35418
31	245	15.9	346	6	US-10-449-902-40549
32	243	15.8	219	6	US-10-471-571A-2420
33	243	15.8	253	6	US-10-471-571A-3050
34	242	15.7	651	6	US-10-471-571A-252
35	240.5	15.6	260	6	US-10-471-571A-2720
36	238	15.4	262	7	US-11-174-307B-3916
37	237	15.4	263	6	US-10-953-349-6892
38	234.5	15.2	1187	7	US-11-056-355B-73529
39	234.5	15.2	1216	7	US-11-056-355B-73528
40	234.5	15.2	1227	7	US-11-056-355B-73527
41	234.5	15.2	1258	7	US-11-056-355B-85264
42	234.5	15.2	1287	7	US-11-056-355B-85263
43	234.5	15.2	1298	7	US-11-056-355B-85262
44	233	15.1	1199	7	US-11-056-355B-83585
45	233	15.1	1213	7	US-11-056-355B-83584

ALIGNMENTS

RESULT 1

US-10-471-571A-3584
; Sequence 3584, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:

; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026297WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: Seqwin99, version 1.03
; SEQ ID NO 3584
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(231)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-3584

Query Match 26.7%; Score 411.5; DB 6; Length 231;
Best Local Similarity 37.3%; Pred. No. 1.5e-21;
Matches 84; Conservative 61; Mismatches 65; Indels 15; Gaps 4;

Qy	4	LLEKNVSKTIRGKKII	EGLSFQVRAGEIFGFLGPNAGAKTTTIRMIVGHMSITAGETAV	63
Db	3	VLTIHLTKIGNKTI	LEDVSVFKLRGQIVGLVGANGAGKTLMLKVLGYSSFOGPNV	62
Qy	64	CGSVKFNPKAARHGA	IVENPELYKFLTGYNLQOYARMTKGVTKKKIDEIVELVGLK	123
Db	63	I-----NSKDSKSNIGAL	TENPGIYPFMSGYENLK---LLNESKNTQDIDKIVSOLHMD	113
Qy	124	NRINDVKVTYSLGMRQ	RLGALSHDHPKLLILDEPTNGLDPAIGRIEIRDYLRKLTRKGG	183
Db	114	EYHKAKTYSLGMRQ	KGLGIAIAFLNKPQFIIDEPNMGDLPKAVRDRELIVQAE-G	172
Qy	184	MAVIVSHLSELMCD	RIATIQNGKLRDIQHVGHGPARDEKKRY	228
Db	173	VTFLSSHLSELVK	ITNSLIINKGKI-----VTETSEBELKQF	212

RESULT 2

US-10-471-571A-1354
; Sequence 1354, Application US/10471571A

```
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 1354
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(290)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-1354
```

```
Query Match 26.2%; Score 404.5; DB 6; Length 290;
Best Local Similarity 31.2%; Pred. No. 6e-21;
Matches 94; Conservative 76; Mismatches 106; Indels 25; Gaps 8;

QY 5 LELKNVSKTIRGKKIIEGLSFDVRAGEIFGLGPNAGAGKTTTIRMIVGHMSITAGIAVC 64
bb 1 MKLEHITKKYGSNVVNDIDFDGDSRIIVGLIGNGVGKTTVMKVMNGNIIRKFDGKVDI- 59
QY 65 GVSVKENFEKAARHIGAIVENPELYKFLTYGQNLQOYAR-MTKGVTKKKIDEIVELVGLK 123
Db 60 -----DN-----ADNIGFLIEHPKLYDNKSGLYNLKLFQAVLKGKFDKAVTDKIIDAFGMR 110
QY 124 NRINDKVTYSLGMRQRLGQAQLLHDPKLLIIDEPTNGLDPDAGIREIRDYLRKLTREG 183
Db 111 PYIKKKVKYSGMKQKLAIAVSLMKNPKPLIILDEPTNGMDPDGSDIVLTITKSLNELD 170
QY 184 MAVIVSHLLSEMELMCDRIAIONGK-LRDIQHVHGPARD-----EKRYVYIQADDTQ 236
Db 171 MRILSHKLEDIELICDRAVFRDGHFQVDVNMEEGVASDTTIVTVDHKDF-----DRTE 226
QY 237 ALTREAAAFKVKVDRAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLE 296
Db 227 KYLAE--HFQLQNVDRADGHLMINAQKN-YQVILKALSELDIYPKVIETRKSSLRDTYFN 283
QY 297 I 297
Db 284 I 284
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```
RESULT 3
US-10-471-571A-716
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 716
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(232)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-716
```

```
Query Match 25.5%; Score 392.5; DB 6; Length 232;
Best Local Similarity 38.0%; Pred. No. 3e-20;
Matches 79; Conservative 55; Mismatches 69; Indels 5; Gaps 3;

QY 5 LELKNVSKTIRGKKIIEGLSFDVRAGEIFGLGPNAGAGKTTTIRMIVGHMSITAGIAVC 64
Db 6 LVTENISKRFKNQDVLKHINITLENNEVYGLLGINAGAKTTLMKIKCGILQODSGGSIKLD 65
QY 65 GVSVKENFEKAARHIGAIVENPELYKFLTYGQNLQOYARMTKGVTKKKIDEIVELVGLKN 124
Db 66 NRPMTRN---DLHKVGS LIETATYVNHLSAQDNL-KIVCLNESVDSEINSVLSLVNLNV 121
QY 125 RINDKVTYSLGMRQRLGQAQLLHDPKLLIIDEPTNGLDPDAGIREIRDYLRKLTREGKM 184
Db 122 DKKKVKVDFSLGMKQRLGAMALIKKPEILVLDPSNGLDPYGIQELRELLKLT-EQGT 180
QY 185 AVIVSHLLSEMELMCDRIAIONGKLR 212
Db 181 SIIISSHLSEIQVLADHIGIIEGELK 208
```

```
RESULT 4
US-11-293-697-4274
; Sequence 4274, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4274
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4274
```

```
Query Match 22.7%; Score 349.5; DB 7; Length 558;
Best Local Similarity 30.2%; Pred. No. 9e-17;
Matches 101; Conservative 68; Mismatches 108; Indels 57; Gaps 13;

QY 4 LLELKNVSKTIRGKKI--IEGLSFDVRAGEIFGLGPNAGAGKTTTIRMIVGHMSITAGEI 61
Db 204 VLVLRLNLTKYRGQRMPAVDRCLGIPPGECFLLGVNGAGKTSTFRMTGTDLASRGEA 263
QY 62 AVCGSVSVKENFEKAARHI--GAIVENPELYKFLTYGQNLQOYARMTKGVTKKKIDEI--- 116
Db 264 VLAGHSVAR--EPSAAHLSMGYCPQSDAIFELLTGREHLELLARL-RGVPEAQVAQTGS 320
QY 117 -VELVGLKNRINDKVTYSLGMRQRLGQAQLLHDPKLLIIDEPTNGLDPDAGIREIRDYL 175
Db 321 GLARGLSLYADRPAGTYSGGNKRKLATALAVDPFAVFLDDEPTTGMDPSARRFLWNSL 380
QY 176 RKLTRKGMNAVIVSSHLLSEMELMCDRIAIONGKLRDI---QHVHG----- 219
Db 381 LAVVRE-GRSVMLTSHSMECEALCSRLAIWNGRFRCLGSPQHLKGRFAAGHTLTLRVP 439
QY 220 PARDEKKRYIQADDTQALTREAAAFKVKVDRAEGGIELSIQKDEVP----- 267
Db 440 AARSQPAFAAFV-----AAEFPGAELREAHGG-RLRFQ---LPPGRCALARVFG 484
QY 268 DLIKHLTDSGVRLYEVKAVNKSLEDRFLEITADK 301
Db 485 ELAVHGAERHGVDFSVS--QTMLEEVFLYFSKQD 516

RESULT 5
US-11-289-102-341
```

; Sequence 341, Application US/11289102
; Publication No. US20060121511A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
; TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 341
; LENGTH: 1704
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-341

Query Match 22.5%; Score 346.5; DB 7; Length 1704;
Best Local Similarity 32.8%; Pred. No. 6.2e-16;
Matches 105; Conservative 58; Mismatches 126; Indels 31; Gaps 12;
QY 1 LETLLEKNVSKTIRGK--KITEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSIT 57
DB 1377 LHTPLIKELSKRYEQRVPLADRLSLAVQKCEGFLGPNAGAGKTTTIFMLTGESLT 1436
QY 58 AGEIACVGVSVKENFEKAARHIGAIVENPELYKFLTYQNLQOYARMKGVTKKKIDEIV 117
DB 1437 SGDAFVGHRISDVGVQRIGYCPQFDALLDHTGEMLMVMYARL-RGIPERHICACV 1495
QY 118 E--LVG--LKNRINDKVTYSLGMORQLGASLLHDPKLLILDEPTNGLDPAIGIREIRD 173
DB 1496 ENTLRGLLEPHANKLVRTYSGGNKRLSTGIALIGEPVIFLDEPSTGMDPVARRLLWD 1555
QY 174 YLRKLREKGMVIVSSHLLSEMELMCDRIAIIQNGKLDI---QVHGP-ARDEKKRY 229
DB 1556 TVAR-ARESGKALIIITSHSEECALCTRLAIWQGFQKLGSPQHLKSKFGSGYSIRAK 1614
QY 230 IQADDTQALTREAAAF-----RKVKVDEAG-----GIELSIQKDEVPDLIKHLTDS 276
DB 1615 VQSEGQQAEEFAKFVDLTFPGSVLEDEHQGMVHYHLPCRDLSWAK--VFGILEKAKEK 1672
QY 277 -GURLYEVKAVNKSLEDRFL 295
DB 1673 YGVDDYSVSQI--SLEQVFL 1690

RESULT 6
US-10-471-571A-4370
; Sequence 4370, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: Seqwin99, version 1.03
; SEQ ID NO 4370
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(299)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-4370

Query Match 21.9%; Score 338; DB 6; Length 299;
Best Local Similarity 30.5%; Pred. No. 2.5e-16;
Matches 94; Conservative 70; Mismatches 122; Indels 22; Gaps 11;
QY 5 LELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSITAGEIACV 64
DB 3 LVIEHVTKRFQKWTAVNDISLKLESGKMLGFLGRNGAGKTTTFRMILGLSPTGHTYIN 62
QY 65 GUSVKNFEKAARHIGAIVENPELYKFLTYQNLQOYARMKGVTKKKIDEIV---ELV 120
DB 63 G---KKLDKTMVNRIGYLPPEERGLHGKLTVEBEL--KYLATLKGMSKTEIQOISYWLERF 118
QY 121 GLKNRINDKVTYSLGMORQLGASLLHDPKLLILDEPTNGLDPAIGIREIRDYLRKLTR 180
DB 119 DITENRKRIDSLSKGNQKQIQLASMLHKEPELLIDEPFSGLDPVNVELLKEAVKOL-N 177
QY 181 EKGMAVIVSSHLLSEMELMCDRIAIIQNGKLDI---RDIQHVHGPARDKKRYIIQADDT-Q 236
DB 178 DMGSTIVYSSHRMEHVEELCDDVCILDKGQLVVGSDINHVR--ASNGNKKVVISETTLP 235
QY 237 ALTREAAAFKRVKVDENAGGIELSIQKDEV-PDLIKHLTDSG-VRLYEVKAVNKSLEDRF 294
DB 236 DLTNIRGI---IHSENKQGLQLTENEDVAKDIYQVVAHQYVYKRFQV--VEPSLODIF 290
QY 295 LEITADKE 302
DB 291 IEKVGKRD 298

RESULT 7
US-10-449-902-43324
; Sequence 43324, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43324
; LENGTH: 949
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-43324

Query Match 21.5%; Score 331.5; DB 6; Length 949;
Best Local Similarity 29.4%; Pred. No. 3.2e-15;
Matches 96; Conservative 75; Mismatches 120; Indels 35; Gaps 12;
QY 9 NVSKTIRGKK-----IIEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSITAGEIA 62
DB 631 DLKKVYHKGDNPDKEAVRGLSLALPYGECGLGILGPNAGACKSFISMIGLTRPSTGNF 690
QY 63 VCGSVKENFEKAARHIGAIVENPELYKFLTYQNLQOYARMKGVTKKKIDEIV-ELVG 121
DB 691 VREFSTQDMEKIYNSMGVCPQNDMLWEMLTGREHLQFYGRLL--KSLNGSLDFAVNESLR 749
QY 122 LKNRIN---DK-VKTYSLGMORQLGASLLHDPKLLILDEPTNGLDPAIGIREIRDYLR 176
DB 750 SVNLLHGGAPDKQVRKYSGMKRRLSAISLIGDAKVYNDPESTGLDPAIRKSLMDAVK 809
QY 177 KLTRKGMVIVSSHLLSEMELMCDRIAIIQNGKLDI---YITQA---YITQA- 232

Db 810 QAKRDR--AIVLTTHSMEAEVLCRLCIMVDGSLQCI---GTPKELIARYGGYYVLTM 863
 QY 233 -----DQTQALTREAAA-FRKVKYDEAGGIELSIQKDEVPDLIKHLTDSGVRLEYVK 284
 Db 864 TTSPEPEQEVENLARKLSNARKVYHLSGTQKVELPKQVRIADVPM-AVENFKRRTTEVQ 922
 QY 285 A---VNKSLEDFRLEITADKEEAQHV 307
 Db 923 AWGLADTTMEDVFKVAKGQSSEEL 948

RESULT 8
 US-10-449-902-44592
 ; Sequence 44592, Application US/10449902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agrobiological Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A0205Y1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 44592
 ; LENGTH: 949
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; ORGANISM: Oryza sativa
 US-10-449-902-44592

Query Match 21.5%; Score 331.5; DB 6; Length 949;
 Best Local Similarity 29.4%; Pred. No. 3.2e-15;
 Matches 96; Conservative 75; Mismatches 120; Indels 35; Gaps 12;
 QY 9 NVSKTTRGKK-----IIIEGLSPDVRAIGFPGFLGPNAGKTTTIRMIVGHMSITAGEIA 62
 Db 631 DLKKVYHGKDNPKDFAVRGLSALPYGBCGLTGLGPNAGKSSFISMIGLTRPTSGNAF 690
 QY 63 VCGSVKENFEKAARHIGAIVENPELYKFLTGYNLQOQYARMTKGVTKKKIDIV-ELVG 121
 Db 691 VREFSIQTWEKIYNSGVCPQNDMLWMLTGREHLOFYGRLL-KSLNGSDLDTAVNESLR 749
 QY 122 LKNRIN---DK-VKTYSLGMRQRLGLAOSLLHDPKLLILDEPTNGLDPAGIREIRDYLR 176
 Db 750 SVNLLHGGAPDKQVKYSGMKRRLSVAISLIGDAKVVMYDEPSTGLDPASRKSILDAVK 809
 QY 177 KLTREGMAVIVSHLLSEMELMCDRIAIIONGKLRDIQHVHGPARDEKKR-----YIIQA- 232
 Db 810 QAKRDR--AIVLTTHSMEAEVLCRLCIMVDGSLQCI---GTPKELIARYGGYYVLTM 863
 QY 233 -----DQTQALTREAAA-FRKVKYDEAGGIELSIQKDEVPDLIKHLTDSGVRLEYVK 284
 Db 864 TTSPEPEQEVENLARKLSNARKVYHLSGTQKVELPKQVRIADVPM-AVENFKRRTTEVQ 922
 QY 285 A---VNKSLEDFRLEITADKEEAQHV 307
 Db 923 AWGLADTTMEDVFKVAKGQSSEEL 948

RESULT 9
 US-11-274-683-30
 ; Sequence 30, Application US/11274683
 ; Publication No. US20060141583A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Haitli, Bradley A
 ; TITLE OF INVENTION: Elaiophyllin biosynthetic gene cluster

FILE REFERENCE: 1855/256
 ; CURRENT APPLICATION NUMBER: US/11/274,683
 ; CURRENT FILING DATE: 2005-11-14
 ; PRIOR APPLICATION NUMBER: US 60/627,752
 ; PRIOR FILING DATE: 2004-11-12
 ; NUMBER OF SEQ ID NOS: 55
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 30
 ; LENGTH: 304
 ; TYPE: PRT
 ; ORGANISM: Streptomyces sp. NRRL 30748
 ; ORGANISM: Streptomyces sp. NRRL 30748
 US-11-274-683-30

Query Match 20.5%; Score 316.5; DB 7; Length 304;
 Best Local Similarity 27.9%; Pred. No. 7.8e-15;
 Matches 89; Conservative 64; Mismatches 125; Indels 41; Gaps 8;
 QY 4 LLELKNVSKTTRGKKIIIEGLSPDVRAIGFPGFLGPNAGKTTTIRMIVGHMSITAGEIAV 63
 Db 3 LIEVSNLRKEYRNHVAQDVFSVEEGEIFGLGPNAGKTTTAVCEICGMKRKRDGGEISV 62
 QY 64 CGSVKENFEKA--ARHIGAIVENPELYKFLTGYNLQOQYARMTKGVTKKKID--EIVEL 119
 Db 63 MGLDPLKOKDLAELRESIGIQQSELPPKMKVWEALELYSTF----YRDPVDWRLEIKD 118
 QY 120 VGLKNRINDKVITYSLGMRQRLGLAOSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLT 179
 Db 119 WGLSDKADTAYGSLSGGQQQRLSIALALVGPRIAVFDELTTALDPPHARRETWKLEKV- 177
 QY 180 REKGMVIVSHLLSEMELMCDRIAIIONGKLRDIQHVHG-----PAR 222
 Db 178 REQDVTLLVTHFMEAEERLCRIAIIESGRVVALDTPSLGVSRLVDEQQIIRPKSPVPM 237
 QY 223 DEKKRYIQADDTQALTREAAA-FRKVKYDEAGGIELSIQKDEVPDLIKHLTDSGVRLEY 282
 Db 238 DE---LLTSLPEVSVTRSKSQVTVV----GKGNVYAV-----ISVLARNQIVANE 282
 QY 283 KVANKNSLEDFRLEITADK 301
 Db 283 LRLEQASLDLDAFVALTGSK 301

RESULT 10
 US-10-449-902-54801
 ; Sequence 54801, Application US/10449902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agrobiological Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A0205Y1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 54801
 ; LENGTH: 968
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; ORGANISM: Oryza sativa
 US-10-449-902-54801

Query Match 20.5%; Score 315.5; DB 6; Length 968;
 Best Local Similarity 36.3%; Pred. No. 4.1e-14;
 Matches 73; Conservative 43; Mismatches 76; Indels 9; Gaps 4;
 QY 20 IEGLSPDVRAIGFPGFLGPNAGKTTTIRMIVGHMSITAGEIAVCGSVKKE--NFEKAAR 77

Db 549 VKGLWNLKDLQFLGLPAGAGKTTTISCITGITPTGDMYIGHSVRSTAGSMNRR 608
QY 78 HIGAIENPELYKFLTCYQNLQOYARMTKGVTKKKIDIVE-----LVGLKRNINDKVKTY 133
Db 609 MIGVCPDFDILMDALTAKEHMFASI-KGLPPSTIKSVABQSILQVKLSQAAVNRAGSY 667
QY 134 SLGMRORGLAQSLLHDPKLLILDEPTNGDPPAGIREIRDYLRKLTREKGMVIVSSHLL 193
Db 668 SGMKRLSVAIALIGDPKLVFLDEPTTGMDFTRRHVWDIEB-AKKGRAIVLTHSM 725
QY 194 SEMELMCDRIAIQNGKLRDI 214
Db 726 BEADILSDRIAINAKGLRCCI 746

RESULT 11

US-11-293-697-4238
; Sequence 4238, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4238
; LENGTH: 815
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4238

Query Match 20.4%; Score 314; DB 7; Length 815;
Best Local Similarity 30.7%; Pred. No. 4.2e-14;
Matches 96; Conservative 62; Mismatches 115; Indels 40; Gaps 10;

QY 15 RGKKI-IEGLSFDVRAGEIFGLPAGAGKTTTIRMIVGHMSITAGIAVCGSVSKENFE 73
Db 495 RKKKIAARNISFCVQEGEILGLLPGSGAGKSSIRMSITGTTKPTAGEVLKGC----- 548
QY 74 KAARHIGAIENPELYKFLTCYQNLQOYARMTKGVTK-----KIDEIVELVGLKNRINDK 129
Db 549 SVLGHGVCQENLWPMPLTRHELVYAAV-KGLRKADARLAIALVSAFKLHQLNVP 607
QY 130 VKTYSGLMRORGLAQSLLHDPKLLILDEPTNGDPPAGIREIRDYLRKLTREKGMVIVS 189
Db 608 VQKLTAGITRKLCLFVLSLLGNSPVLDDPESTGIDPTGQOQMQAQVAVKNTERGVLTT 667
QY 190 SHLLSEMELMCDRIAIQNGKLR-----DIQHVHGARDKKRYI-----QADDTQALTRAA 243
Db 668 THNLAEALCDRAIVMSVRLCIGSIQHL-----KNKLGKQVILELKVETSKQVTLVHT 723
QY 244 AFRKVKVDEA-EGGIELSQKDEVDL-----IKHLTDSGVLYEYKAVNKS 289
Db 724 EILKLPQAAGQRYSSLLTKLPVADVPLSQTFFHKLAVKH-----NFNLEBSYSQCT 779
QY 290 LEDRFLEITADKE 302
Db 780 LERVLELSKEQE 792

RESULT 12

US-11-293-697-2603
; Sequence 2603, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697

; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2603
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2603

Query Match 19.7%; Score 303.5; DB 7; Length 559;
Best Local Similarity 28.9%; Pred. No. 1.4e-13;
Matches 88; Conservative 73; Mismatches 115; Indels 29; Gaps 10;

QY 23 LSPDVRAGEIFGLPAGAGKTTTIRMIVGHMSITAGIAVCGSVSK-ENFEKAARHIGA 81
Db 236 ISFCVKKGEILGLLPGAGKSTIINILVGDIEPTSGQVFLGDYSSSETSEDDSLKCMGY 295
QY 82 IVENPELYKFLTCYQNLQOYARMTKGV-----KKKIDEIVELVGLKNRINDKVKTYSIGM 137
Db 296 CPQINLWPDPTTLOSHFEIYGAV-KGMSASDMKEVISRITHALDLKHLQKTVKKLPAGI 354
QY 138 RQRGLAQSLLHDPKLLILDEPTNGDPPAGIREIRDYLRKLTREKGMVIVSSHLLSEME 197
Db 355 KRKLCFALSMLGNPQITLLDEPSTGMDPKAKQHMWRRAIRTAFAKVRKRAAILTTHYMBEAE 414
QY 198 LMCDRIAIIONKLR-----DIQHV-----HGPARDEKKRYIQAODTQALTRAA-APRKV 248
Db 415 AVCDRVAIMVSGQLRCIGTQVHLKSKFGKGYFLKIKLMDWENLEVDRLQREIQVIPPNA 474
QY 249 KVDEAEGGIELSQKDEVP-DLIKHLTDSGVLYEYVK-----AVNK-----SLEDRELEIT 298
Db 475 SROESFS-----SILAHKIPKEDVQSLSQSPFKLEBAKHAFAIBEYSFSQATLEQVVELT 530
QY 299 ADKEE 303
Db 531 KEQEE 535

RESULT 13

US-10-471-571A-3086
; Sequence 3086, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3086
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(325)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-3086

Query Match 19.6%; Score 301.5; DB 6; Length 325;
Best Local Similarity 27.2%; Pred. No. 9.2e-14;
Matches 89; Conservative 72; Mismatches 139; Indels 27; Gaps 9;

QY 4 LLELKNVSKTIRKGIIEGLSFDVRAGEIFGLPAGAGKTTTIRMIVGHMSITAGIAV 63
Db 1 VIKPKVTKRYGKHVAVDNISFNINEGEPFVLGPGSCGKTTTLKMINLIHLESEGIYF 60
QY 64 CGSVSKENFEKAAR-HIGAIENPELYKFLTCYQNLQOYARMTKGVTK---KKIDEIVEL 119

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Db      61 KDRPIGDYVYEMRWIDGYVLOQIALFPHTMTIKENIAQVPMKKWKEKDIDKRVDELLEM 120
Qy      120 VGL-----KQRIKNDKVTYSLGMRORLGLAQSLHDPKLLILDEPTNGLDPAQIRIRDY 174
Db      121 VGLPEPKYKPKDEL---SGGQRQVGVIRALAADPPVILMDPEPFSALDPTISREKLQDD 177
Qy      175 LRKLTRKGNMAVIVSHLLSEMELMCDRIAIIQNGKLRDITQHVHGPARDEKKRYIIQ--- 231
Db      178 LIELQTKIKKTIIFVTHDQEMKLGDKICLLNEGHEIQIDTPEGFKNNPQSEFVKQFMG 237
Qy      232 --ADDOALTRAAAFKRV---KVDEAEGGIELSTQKDEVP-DLIKHLTDSGVRLYEVK 284
Db      238 SHLEDDAPCVENAIRDLIDMKPIDEVITMSAYPIYDNQPTIEVLYQLLSSESRVIMVQ 297
Qy      285 --AVNKSLEDR---FLEITADKEEAQH 306
Db      298 EDSVGQYVIDRKDIFKYLQKKEVAQH 324
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RESULT 14

```
US-10-471-571A-2868
; Sequence 2868, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927W0
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 2868
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(341)
; OTHER INFORMATION: ABC transporter ATP-binding
US-10-471-571A-2868
```

```
Query Match      19.2%; Score 296.5; DB 6; Length 341;
Best Local Similarity 30.4%; Pred. No. 2.2e-13;
Matches 73; Conservative 55; Mismatches 97; Indels 15; Gaps 4;

Qy      4 LLELKNVSKTIRGKK----IIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAG 59
Db      1 VIELKEVVEYRTKNKEVLAVDHVNLISIRAGSIYGVIFSGAGKSTLIRMFNHLAPTS 60
Qy      60 EIAVCGSV---KENFEKAARHIGAIVENPELYKFLTYQNLQ---QYARMTKGVTKKX 112
Db      61 EVIIDGHIQGLSKNGLRKRAKQKQVSMIFQHFNLMSRTVLKNI MFLEIAGVPRRAKQK 120
Qy      113 IDEIVELVGLKRNINDKVTYSLGMRORLGLAQSLHDPKLLILDEPTNGLDPAQIREIR 172
Db      121 ALELVGLVGLKREKAYPSLSGGQKQKQVGIARALANDPTVLLCDEATSDALDPTTDEIL 180
Qy      173 DYLRKLTREKGMVIVSSHLLSEMELMCDRIAIIQNGKLRD----IQHVHGPARDEKKRY 228
Db      181 DLLLKIREQNLTVLITHEMHVIRRICDEVAVMESGKVEIQGPVTVQVFENPQHTVTKRF 240
```

RESULT 15

```
US-10-471-571A-678
; Sequence 678, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927W0
```

```
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 678
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(256)
; OTHER INFORMATION: ABC transporter ecsA
US-10-471-571A-678
```

```
Query Match      19.1%; Score 294; DB 6; Length 256;
Best Local Similarity 28.5%; Pred. No. 2.2e-13;
Matches 68; Conservative 62; Mismatches 87; Indels 22; Gaps 5;

Qy      16 GK-KIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGIACVGVSVKENFEK 74
Db      23 GKRPVIKIDINFELNKGIEIVGLIGLNGAGKSTTIKHMGLLTPMEGSLISIDINDDIEA 82
Qy      75 AARHIGAIVENPELYKFLTYQNLQYARMT-----KGVTKKKIDEIVELVGLKNRIN 127
Db      83 YRKLSYIPESPVIYEELT---LESHIEMTAMAYDIDRDETNNRAMPLLTFRLENELK 138
Qy      128 DKVKTYSLGMRORLGLAQSLHDPKLLILDEPTNGLDPAQIREIRDYLRKLTRKGNMAVI 187
Db      139 VFPFSFKGMKQKVMICAFIVNPELYIIDEPFLGDLDPGLIQSLMDLMVE-KKNEGRTVL 197
Qy      188 VSSHLLSEMELMCDRIAIIQNGK-----LRDIQHVHGPARDEKKRYIIQADDTQA 237
Db      198 MSTHILATAERYCDRFIILDEGEVWAFGDLEALRQQTGLHNTLDDIYIHVTOGGDVHA 256
```

Search completed: July 13, 2006, 13:54:27
Job time : 30 secs